

142.2

Best-BlastP=> >nrprot 62% Identities = 108/225 (48%), Positives = 144/225 (64%), Gaps = 1/225 (0%) ref|NP_455898.1| D-alanyl-D-alanine dipeptidase [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_805294.1| D-alanyl-D-alanine dipeptidase [Salmonella enterica subsp. enterica serovar Typhi (strain CT18) emb|CAD01726.1| D-alanyl-D-alanine dipeptidase [Salmonella enterica subsp. enterica serovar Typhi] gbl|AA06143.1| D-alanyl-D-alanine dipeptidase [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 256

1420.2 Best-BlastP=> >nrprot 80% Identities = 258/380 (67%), Positives = 309/380 (81%) ref|NP_820998.1| cystathionine beta-lyase [Coxiella burnetii RSA 493] gbl|AAO91512.1| cystathionine beta-lyase [Coxiella burnetii RSA 493] Length = 387

1421.3 Best-BlastP=> >nrprot 55% Identities = 280/736 (38%), Positives = 432/736 (58%), Gaps = 19/736 (2%) ref|NP_900703.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gbl|AAQ58708.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 936

1423.2 Best-BlastP=> >nrprot 66% Identities = 226/450 (50%), Positives = 315/450 (70%), Gaps = 2/450 (0%) pirl|JC5798 F0F1-ATPase (EC 3.4.-.) beta chain - Methanosaarcina barkeri gbl|AAC38049.1| ATP synthase beta subunit [Methanosaarcina barkeri] Length = 469

1424.2 Best-BlastP=> >nrprot 37% Identities = 27/106 (25%), Positives = 51/106 (48%) ref|ZP_00090544.1| COG0355: F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit) [Azotobacter vinelandii] Length = 178

1425.2 Best-BlastP=> >nrprot 50% Identities = 25/88 (28%), Positives = 47/88 (53%), Gaps = 2/88 (2%) ref|NP_661922.1| ATP synthase, putative [Chlorobium tepidum TLS] gbl|AAM72264.1| ATP synthase, putative [Chlorobium tepidum TLS] Length = 107

1429.4 Best-BlastP=> >nrprot 26% Identities = 68/329 (20%), Positives = 131/329 (39%), Gaps = 32/329 (9%) emb|CAD27470.1| SPAPB18E9.04c [Schizosaccharomyces pombe] Length = 800

1432.3 Best-BlastP=> >nrprot 52% Identities = 105/294 (35%), Positives = 160/294 (54%), Gaps = 6/294 (2%) ref|NP_745744.1| transcriptional regulator, LysR family [Pseudomonas putida KT2440] gbl|AAN69208.1|AE016555_6 transcriptional regulator, LysR family [Pseudomonas putida KT2440] Length = 309

1434.3 Best-BlastP=> >nrprot 52% Identities = 242/765 (31%), Positives = 388/765 (50%), Gaps = 49/765 (6%) ref|NP_842403.1| DNA internalization-related competence protein ComEC/Rec2 [Nitrosomonas europaea ATCC 19718] emb|CAD86320.1| DNA internalization-related competence protein ComEC/Rec2 [Nitrosomonas europaea ATCC 19718] Length = 799

1438.4 Best-BlastP=> >nrprot 80% Identities = 428/631 (67%), Positives = 504/631 (79%), Gaps = 6/631 (0%) ref|NP_245307.1| ParE [Pasteurella multocida] gbl|AAK02454.1| ParE [Pasteurella multocida] Length = 632

144.3 Best-BlastP=> >nrprot 8% Identities = 21/50 (42%), Positives = 31/50 (62%), Gaps = 1/50 (2%) ref|NP_618108.1| cysteine protease (papain C1 family) [Methanosaarcina acetivorans str. C2A] gbl|AAAM06558.1| cysteine protease (papain C1 family) [Methanosaarcina acetivorans str. C2A] Length = 340

1440.2 Best-BlastP=> >nrprot 55% Identities = 163/398 (40%), Positives = 231/398 (58%), Gaps = 45/398 (11%) ref|NP_820093.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] gbl|AAO90607.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] Length = 380

1444.3 Best-BlastP=> >nrprot 46% Identities = 189/523 (36%), Positives = 282/523 (53%), Gaps = 48/523 (9%) ref|NP_775139.1| sphingosine-1-phosphate lyase [Rattus norvegicus] emb|CAD55407.1| sphingosine-1-phosphate lyase [Rattus norvegicus] Length = 568

1446.3 Best-BlastP=>>nrprot 71% Identities = 143/246 (58%), Positives = 181/246 (73%) ref|NP_793532.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57227.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 249

1448.2 Best-BlastP=>>nrprot 50% Identities = 109/334 (32%), Positives = 172/334 (51%), Gaps = 25/334 (7%) ref|NP_106951.1| similar to oxidoreductase [Mesorhizobium loti] dbj|BAB52737.1| similar to oxidoreductase [Mesorhizobium loti] Length = 677

1449.3 Best-BlastP=>>nrprot 52% Identities = 209/735 (28%), Positives = 369/735 (50%), Gaps = 69/735 (9%) ref|ZP_00042382.1| COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1] Length = 726

1450.2 Best-BlastP=>>nrprot 57% Identities = 168/388 (43%), Positives = 244/388 (62%), Gaps = 8/388 (2%) ref|NP_407479.1| multidrug translocase [Yersinia pestis] ref|NP_671360.1| proton motive force efflux pump protein [Yersinia pestis KIM] pir|AD0492 multidrug translocase [imported] - Yersinia pestis (strain CO92) emb|CAC93504.1| multidrug translocase [Yersinia pestis CO92] gb|AAM87611.1|AE014008_5 proton motive force efflux pump protein [Yersinia pestis KIM] Length = 409

1451.4 Best-BlastP=>>nrprot 65% Identities = 188/426 (44%), Positives = 278/426 (65%), Gaps = 4/426 (0%) ref|ZP_00034777.1| COG2252: Permeases [Burkholderia fungorum] Length = 433

1454.2 Best-BlastP=>>nrprot 88% Identities = 500/638 (78%), Positives = 568/638 (89%) ref|NP_901459.1| protein kinase [Chromobacterium violaceum ATCC 12472] Length = 642

1455.2 Best-BlastP=>>nrprot 47% Identities = 52/155 (33%), Positives = 81/155 (52%), Gaps = 10/155 (6%) ref|NP_253150.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] pir|D83087 conserved hypothetical protein PA4460 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07848.1|AE004860_4 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 175

1456.2 Best-BlastP=>>nrprot 80% Identities = 165/238 (69%), Positives = 194/238 (81%) ref|NP_719490.1| ABC transporter, ATP-binding protein [Shewanella oneidensis MR-1] gb|AAN56934.1|AE015827_6 ABC transporter, ATP-binding protein [Shewanella oneidensis MR-1] Length = 243

1457.2 Best-BlastP=>>nrprot 73% Identities = 105/185 (56%), Positives = 141/185 (76%), Gaps = 1/185 (0%) ref|ZP_00079751.1| COG0512: Anthranilate/para-aminobenzoate synthases component II [Geobacter metallireducens] Length = 189

1461.3 Best-BlastP=>>nrprot 68% Identities = 167/315 (53%), Positives = 214/315 (67%), Gaps = 20/315 (6%) ref|NP_819187.1| UDP-N-acetylendopyruvoylglucosamine reductase [Coxiella burnetii RSA 493] gb|AAO89701.1| UDP-N-acetylendopyruvoylglucosamine reductase [Coxiella burnetii RSA 493] Length = 316

1463.2 Best-BlastP=>>nrprot 66% Identities = 170/375 (45%), Positives = 241/375 (64%), Gaps = 16/375 (4%) ref|NP_773078.1| D-alanine--D-alanine ligase A [Bradyrhizobium japonicum] dbj|BAC51703.1| D-alanine--D-alanine ligase A [Bradyrhizobium japonicum USDA 110] Length = 373

1466.2 Best-BlastP=>>nrprot 71% Identities = 94/205 (45%), Positives = 152/205 (74%) ref|NP_841948.1| Prokaryotic-type carbonic anhydrase [Nitrosomonas europaea ATCC 19718] Length = 208

1467.5 Best-BlastP=>>nrprot 65% Identities = 90/186 (48%), Positives = 126/186 (67%), Gaps = 2/186 (1%) ref|NP_691260.1| hypothetical protein [Oceanobacillus iheyensis HTE831] dbj|BAC12295.1| hypothetical conserved protein [Oceanobacillus iheyensis HTE831] Length = 189

1469.4 Best-BlastP=>>nrprot 20% Identities = 112/493 (22%), Positives = 217/493 (44%), Gaps = 44/493 (8%) ref|NP_563924.1| nuclear matrix constituent protein -related [Arabidopsis thaliana] pir|G86266 hypothetical protein F3F19.25 - Arabidopsis thaliana gb|AAD31075.1|AC007357_24 Similar to gb|D64087 nuclear matrix constituent protein 1 (NMCP1) from Daucus carota. [Arabidopsis thaliana] Length = 1128

1473.4 Best-BlastP=>>nrprot 49% Identities = 44/143 (30%), Positives = 75/143 (52%), Gaps = 4/143 (2%) ref|NP_810648.1| chromate transport protein [Bacteroides thetaiaotamicron VPI-5482] Length = 185

1474.4 Best-BlastP=>>nrprot 52% Identities = 125/314 (39%), Positives = 194/314 (61%), Gaps = 4/314 (1%) ref|NP_103760.1| unknown protein [Mesorhizobium loti] dbj|BAB49546.1| unknown protein [Mesorhizobium loti] Length = 431

1475.2 Best-BlastP=>>nrprot No Hits found

1476.2 Best-BlastP=>>nrprot 81% Identities = 185/302 (61%), Positives = 246/302 (81%), Gaps = 1/302 (0%) ref|NP_762779.1| Glutathione synthase; Ribosomal protein S6 modification enzyme [Vibrio vulnificus CMCP6] gb|AAO07769.1|AE016811_10 Glutathione synthase; Ribosomal protein S6 modification enzyme [Vibrio vulnificus CMCP6] dbj|BAC97337.1| ribosomal protein S6 modification protein [Vibrio vulnificus YJ016] Length = 301

1479.3 Best-BlastP=>>nrprot 69% Identities = 223/407 (54%), Positives = 287/407 (70%), Gaps = 1/407 (0%) spl|Q8GDU5|ARLY_HELMO Argininosuccinate lyase (Arginosuccinase) (ASAL) gb|AN87483.1| Argininosuccinate lyase [Helicobacillus mobilis] Length = 458

148.2 Best-BlastP=>>nrprot 55% Identities = 186/450 (41%), Positives = 279/450 (62%), Gaps = 14/450 (3%) ref|ZP_00060071.1| COG2200: FOG: EAL domain [Clostridium thermocellum ATCC 27405] Length = 862

1481.3 Best-BlastP=>>nrprot 51% Identities = 128/304 (42%), Positives = 191/304 (62%), Gaps = 9/304 (2%) ref|NP_126998.1| ornithine carbamoyltransferase [Pyrococcus abyssi] spl|O93656|OTC_PYRAB Ornithine carbamoyltransferase (OTCase) pir|G75041 ornithine carbamoyltransferase (argF) PAB1502 - Pyrococcus abyssi (strain Orsay) emb|CAB50228.1| argF ornithine carbamoyltransferase [Pyrococcus abyssi] Length = 317

1482.4 Best-BlastP=>>nrprot 22% Identities = 40/150 (26%), Positives = 71/150 (47%) ref|NP_819099.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89613.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 250

1484.2 Best-BlastP=>>nrprot 72% Identities = 126/223 (56%), Positives = 164/223 (73%) ref|ZP_00053873.1| COG1136: ABC-type antimicrobial peptide transport system, ATPase component [Magnetospirillum magnetotacticum] Length = 225

1485.4 Best-BlastP=>>nrprot 64% Identities = 171/414 (41%), Positives = 268/414 (64%), Gaps = 4/414 (0%) ref|NP_436895.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] pir|C95886 conserved hypothetical protein [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymb emb|CAC48755.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] Length = 413

1487.3 Best-BlastP=>>nrprot 99% Identities = 266/268 (99%), Positives = 268/268 (100%) emb|CAB65183.1| enoyl reductase [Legionella pneumophila] Length = 268

1488.2 Best-BlastP=>>nrprot No Hits found

1490.4 Best-BlastP=>>nrprot 72% Identities = 536/927 (57%), Positives = 679/927 (73%), Gaps = 9/927 (0%) ref|NP_819435.1| isoleucyl-tRNA synthetase [Coxiella burnetii RSA 493] gb|AAO89949.1| isoleucyl-tRNA synthetase [Coxiella burnetii RSA 493] Length = 936

1493.6 Best-BlastP=> nrprot 69% Identities = 822/1621 (50%), Positives = 1137/1621 (70%), Gaps = 3/1621 (0%) refNP_820221.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90735.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 1619

1494.2 Best-BlastP=> nrprot 33% Identities = 58/1170 (34%), Positives = 89/1170 (52%), Gaps = 1/170 (0%) refZP_00081963.1| COGG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Geobacter metallireducens] Length = 234

1495.1 Best-BlastP=> nrprot 72% Identities = 60/104 (57%), Positives = 78/104 (75%) refNP_458777.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi] refNP_463202.1| putative DMT superfamily transport protein [Salmonella typhimurium LT2] refNP_807981.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAL23161.1| putative DMT superfamily transport protein [Salmonella typhimurium LT2] emb|CAD06818.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO71841.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 105

1497.2 Best-BlastP=> nrprot 66% Identities = 189/335 (56%), Positives = 236/335 (70%) refZP_00125893.1| COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Pseudomonas syringae pv. syringae B728a] Length = 354

15.1 Best-BlastP=> nrprot 63% Identities = 181/393 (46%), Positives = 248/393 (63%), Gaps = 20/393 (5%) refNP_890078.1| phage integrase [Bordetella bronchiseptica] emb|CAE34037.1| phage integrase [Bordetella bronchiseptica] Length = 407

150.2 Best-BlastP=> nrprot 52% Identities = 130/266 (48%), Positives = 172/266 (64%), Gaps = 8/266 (3%) refZP_00029131.1| COG3243: Poly(3-hydroxyalkanoate) synthetase [Burkholderia fungorum] Length = 642

1501.3 Best-BlastP=> nrprot 72% Identities = 139/276 (50%), Positives = 200/276 (72%), Gaps = 2/276 (0%) refNP_519387.1| PROBABLE SN-GLYCEROL-3-PHOSPHATE TRANSMEMBRANE ABC TRANSPORTER PROTEIN [Ralstonia solanacearum] emb|CAD14968.1| PROBABLE SN-GLYCEROL-3-PHOSPHATE TRANSMEMBRANE ABC TRANSPORTER PROTEIN [Ralstonia solanacearum] Length = 282

1503.4 Best-BlastP=> nrprot 65% Identities = 183/364 (50%), Positives = 239/364 (65%), Gaps = 15/364 (4%) refNP_407240.1| sn-glycerol-3-phosphate transport, ATP-binding protein [Yersinia pestis] pir|AH0461 sn-glycerol-3-phosphate transport, ATP-binding protein ugC [Imported] - Yersinia pestis (strain CO92) embl|CAC93260.1| sn-glycerol-3-phosphate transport, ATP-binding protein [Yersinia pestis CO92] Length = 357

1505.4 Best-BlastP=> nrprot No Hits found

1507.3 Best-BlastP=> nrprot 64% Identities = 226/496 (45%), Positives = 318/496 (64%), Gaps = 4/496 (0%) refNP_231057.1| thermostable carboxypeptidase 1 [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82202 thermostable carboxypeptidase 1 VC1414 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94571.1| thermostable carboxypeptidase 1 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 524

1508.4 Best-BlastP=> nrprot 38% Identities = 85/279 (30%), Positives = 141/279 (50%), Gaps = 9/279 (3%) refNP_622993.1| predicted nucleotide-molybdopterin-biosynthesis enzyme MoeA [Thermoanaerobacter tengcongensis] gb|AM24597.1| predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA [Thermoanaerobacter tengcongensis] Length = 412

151.2 Best-BlastP=>>nprot 70% Identities = 128/248 (51%), Positives = 176/248 (70%), Gaps = 4/248 (1%) ref|NP_902034.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ60036.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] Length = 246

1510.3 Best-BlastP=>>nprot 64% Identities = 136/259 (52%), Positives = 177/259 (68%), Gaps = 1/259 (0%) ref|ZP_00083725.1| COG3186: Phenylalanine-4-hydroxylase [Pseudomonas fluorescens PfO-1] Length = 263

1511.3 Best-BlastP=>>nprot 99% Identities = 217/219 (99%), Positives = 218/219 (99%) gb|AAL79360.1| GacA regulatory protein [Legionella pneumophila] Length = 219

1513.4 Best-BlastP=>>nprot 61% Identities = 181/448 (40%), Positives = 276/448 (61%), Gaps = 20/448 (4%) ref|NP_820336.1| amino acid antiporter [Coxiella burnetii RSA 493] gb|AAO90850.1| amino acid antiporter [Coxiella burnetii RSA 493] Length = 474

1515.2 Best-BlastP=>>nprot 73% Identities = 127/255 (49%), Positives = 188/255 (73%), Gaps = 1/255 (0%) ref|NP_249886.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|F83497 hypothetical protein PA1195 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG04584.1|AE004549_11 hypothetical protein PA1195 [Pseudomonas aeruginosa PAO1] Length = 254

1516.3 Best-BlastP=>>nprot 39% Identities = 69/269 (25%), Positives = 123/269 (45%), Gaps = 14/269 (5%) ref|NP_826905.1| hypothetical protein [Streptomyces avermitilis MA-4680] dbj|BAC73440.1| hypothetical protein [Streptomyces avermitilis MA-4680] Length = 290

1517.3 Best-BlastP=>>nprot 58% Identities = 164/368 (44%), Positives = 244/368 (66%), Gaps = 1/368 (0%) ref|ZP_00034488.1| COG0156: 7-keto-8-aminopelargonate synthetase and related enzymes [Burkholderia fungorum] Length = 429

1519.2 Best-BlastP=>>nprot 53% Identities = 126/333 (37%), Positives = 184/333 (55%), Gaps = 4/333 (1%) ref|ZP_00034487.1| COG0784: FOG: CheY-like receiver [Burkholderia fungorum] Length = 333

152.3 Best-BlastP=>>nprot 50% Identities = 33/120 (27%), Positives = 60/120 (50%), Gaps = 8/120 (6%) ref|NP_459344.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] gb|AAL19303.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] Length = 119

1521.2 Best-BlastP=>>nprot 56% Identities = 69/170 (40%), Positives = 107/170 (62%) ref|NP_541215.1| HDDED PROTEIN [Brucella melitensis] ref|NP_700223.1| conserved hypothetical protein [Brucella suis 1330] pir|AD3539 hdED protein [imported] - Brucella melitensis (strain 16M) gb|AAL53479.1| HDDED PROTEIN [Brucella melitensis 16M] gb|AAN34228.1|AE014598_9 conserved hypothetical protein [Brucella suis 1330] Length = 187

1522.2 Best-BlastP=>>nprot 32% Identities = 77/231 (33%), Positives = 127/231 (54%), Gaps = 1/231 (0%) ref|NP_691224.1| hypothetical protein [Oceanobacillus iheyensis HTE831] dbj|BAC12259.1| hypothetical conserved protein [Oceanobacillus iheyensis HTE831] Length = 243

1523.2 Best-BlastP=>>nprot No Hits found

1524.3 Best-BlastP=>>nprot 21% Identities = 48/129 (37%), Positives = 76/129 (58%), Gaps = 4/129 (3%) ref|NP_561262.1| probable transcriptional regulator [Clostridium perfringens] dbj|BAB80052.1| probable transcriptional regulator [Clostridium perfringens str. 13] Length = 249

1525.3 Best-BlastP=>>nprot 51% Identities = 137/384 (35%), Positives = 217/384 (56%), Gaps = 24/384 (6%) gb|AAM73854.1|AF454865_1 putative phospholipase C [Legionella pneumophila] Length = 423

1528.4 Best-BlastP=>>nrprot 65% Identities = 214/446 (47%), Positives = 291/446 (65%), Gaps = 6/446 (1%) ref|Q8PMU6|RUMA_XANAC 23S rRNA
(Uracil-5-)-methyltransferase rumA (23S rRNA)(M-5-U1939)-methyltransferase) Length = 444

1529.2 Best-BlastP=>>nrprot 77% Identities = 253/394 (64%), Positives = 309/394 (78%) ref|NP_416880.1| putative aminotransferase [Escherichia coli K12] ref|P77434|YFDZ_ECOLI Hypothetical aminotransferase yfdZ pir||H65011 probable transaminase (EC 2.6.1.-) b2379 [similarity] - Escherichia coli (strain K-12) gb|AAC75438.1| putative aminotransferase [Escherichia coli K12] dbj|BAA16249.1| PROBABLE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT). [Escherichia coli] Length = 412

153.2 Best-BlastP=>>nrprot 99% Identities = 436/437 (99%), Positives = 437/437 (100%) ref|NP_819878.1| conserved hypothetical protein [Coxiella burnetii pneumonia] Length = 445

1530.2 Best-BlastP=>>nrprot 52% Identities = 38/108 (35%), Positives = 64/108 (59%) ref|NP_819878.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90392.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 123

1531.3 Best-BlastP=>>nrprot 71% Identities = 360/746 (48%), Positives = 523/746 (70%), Gaps = 17/746 (2%) ref|ZP_00126361.1| COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Pseudomonas syringae pv. syringae B728a] Length = 747

1532.3 Best-BlastP=>>nrprot 52% Identities = 217/688 (31%), Positives = 341/688 (49%), Gaps = 49/688 (7%) ref|NP_249777.1| flagellar hook-associated protein 1 FlgK PAO1 pir||D83511 flagellar hook-associated protein 1 FlgK PA1086 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04475.1|AE004539_17 flagellar hook-associated protein 1 FlgK [Pseudomonas aeruginosa PAO1] Length = 683

1533.1 Best-BlastP=>>nrprot 52% Identities = 120/413 (29%), Positives = 218/413 (52%), Gaps = 12/413 (2%) ref|NP_718794.1| flagellar hook-associated protein FlgL [Shewanella oneidensis MR-1] gb|AAN56238.1|AE015761_8 flagellar hook-associated protein FlgL [Shewanella oneidensis MR-1] Length = 403

1536.3 Best-BlastP=>>nrprot 59% Identities = 259/616 (42%), Positives = 374/616 (60%), Gaps = 9/616 (1%) ref|NP_900243.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58249.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] Length = 621

1539.2 Best-BlastP=>>nrprot No Hits found

154.1 Best-BlastP=>>nrprot 98% Identities = 312/322 (96%), Positives = 317/322 (98%) ref|NP_000621.1| chemiosmotic efflux system C protein B [Legionella pneumonia] Length = 322

1542.2 Best-BlastP=>>nrprot 63% Identities = 161/342 (47%), Positives = 225/342 (65%), Gaps = 5/342 (1%) ref|NP_820833.1| enoyl-CoA hydratase/isomerase family protein [Coxiella burnetii RSA 493] gb|AAO91347.1| enoyl-CoA hydratase/isomerase family protein [Coxiella burnetii RSA 493] Length = 356

1545.3 Best-BlastP=>>nrprot 74% Identities = 319/546 (58%), Positives = 411/546 (75%), Gaps = 7/546 (1%) ref|NP_745048.1| glutaminy-ltRNA synthetase [Pseudomonas putida KT2440] gb|AAQ68512.1|AE016483_3 glutaminy-ltRNA synthetase [Pseudomonas putida KT2440] Length = 567

1547.2 Best-BlastP=>>nrprot 66% Identities = 132/266 (49%), Positives = 182/266 (68%), Gaps = 2/266 (0%) ref|NP_520102.1| PROBABLE TRYPTOPHAN SYNTHASE (ALPHA CHAIN) PROTEIN [Ralstonia solanacearum] ref|CAD15683.1| PROBABLE TRYPTOPHAN SYNTHASE (ALPHA CHAIN) PROTEIN [Ralstonia solanacearum] Length = 265

1548.2 Best-BlastP=> >nrprot 55% Identities = 83/198 (41%), Positives = 129/198 (65%), Gaps = 1/198 (0%) ref|NP_8666390.1| ATP synthase a subunit [Pirellula sp.] emb|CAD78171.1| ATP synthase a subunit [Pirellula sp.] Length = 228

1549.1 Best-BlastP=> >nrprot 66% Identities = 46/73 (63%), Positives = 61/73 (83%) ref|ZP_00034461.1| COG0636: F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K [Burkholderia fungorum] Length = 82

1550.2 Best-BlastP=> >nrprot 50% Identities = 63/254 (24%), Positives = 125/254 (49%), Gaps = 10/254 (3%) ref|NP_617341.1| H(+)-transporting ATP synthase, subunit B [Methanosc礼ina acetivorans str. C2A] gb|AAM05821.1| H(+)-transporting ATP synthase, subunit B [Methanosc礼ina acetivorans str. C2A] Length = 329

1552.3 Best-BlastP=> >nrprot 87% Identities = 381/511 (74%), Positives = 452/511 (88%), Gaps = 1/511 (0%) ref|ZP_00065462.1| COG0056: F0F1-type ATP synthase, alpha subunit [Microbulbifer degradans 2-40] Length = 513

1555.2 Best-BlastP=> >nrprot 79% Identities = 189/288 (65%), Positives = 231/288 (80%), Gaps = 2/288 (0%) ref|NP_254242.1| ATP synthase gamma chain [Pseudomonas aeruginosa PAO1] pir|D82952 ATP synthase gamma chain PA5555 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAQ08940.1|AE004967_11 ATP synthase gamma chain [Pseudomonas aeruginosa PAO1] Length = 286

1556.2 Best-BlastP=> >nrprot 92% Identities = 395/458 (86%), Positives = 423/458 (92%), Gaps = 1/458 (0%) pir|D64071 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Haemophilus influenzae (strain Rd KW20) Length = 468

1557.3 Best-BlastP=> >nrprot 90% Identities = 227/291 (78%), Positives = 265/291 (91%) ref|NP_820381.1| succinyl-CoA synthetase, alpha subunit [Coxiella burnetii RSA 493] sp|P53591|SUCD_COXBU Succinyl-CoA synthetase alpha chain (SCS-alpha) gb|AAQ090895.1| succinyl-CoA synthetase, alpha subunit [Coxiella burnetii RSA 493] Length = 294

1559.2 Best-BlastP=> >nrprot 80% Identities = 269/384 (70%), Positives = 314/384 (81%) ref|NP_250279.1| succinyl-CoA synthetase beta chain [Pseudomonas aeruginosa PAO1] sp|P53593|SUCC_PSEAE Succinyl-CoA synthetase beta chain (SCS-beta) pir|A83446 succinyl-CoA synthetase beta chain PA1588 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAQ04977.1|AE004587_1 succinyl-CoA synthetase beta chain [Pseudomonas aeruginosa PAO1] Length = 388

1560.2 Best-BlastP=> >nrprot 59% Identities = 115/277 (41%), Positives = 166/277 (59%), Gaps = 11/277 (3%) ref|NP_442598.1| PLeD gene product homologue [Synechocystis sp. PCC 6803] pir|S76977 pLeD-4 protein - Synechocystis sp. (strain PCC 6803) db|BAA10669.1| srl0302 [Synechocystis sp. PCC 6803] Length = 768

1562.3 Best-BlastP=> >nrprot 34% Identities = 51/213 (23%), Positives = 94/213 (44%), Gaps = 27/213 (12%) ref|NP_705294.1| hypothetical protein [Plasmidium falciparum 3D7] emb|CAD52531.1| hypothetical protein [Plasmidium falciparum 3D7] Length = 1936

1563.3 Best-BlastP=> >nrprot 64% Identities = 95/200 (47%), Positives = 134/200 (67%), Gaps = 1/200 (0%) ref|ZP_00087981.1| COG1335: Amidases related to nicotinamidase [Pseudomonas fluorescens PFO-1] Length = 208

1564.3 Best-BlastP=> >nrprot 81% Identities = 321/467 (68%), Positives = 380/467 (81%) ref|NP_820039.1| nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] gb|AAQ090553.1| nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] Length = 468

1566.3 Best-BlastP=> >nrprot 25% Identities = 34/120 (28%), Positives = 47/120 (39%), Gaps = 18/120 (15%) gb|AAQ23913.1| metallothionein IIE [Crassostrea virginica] Length = 149

1567.2 Best-BlastP=> >nrprot 28% Identities = 58/293 (19%), Positives = 127/293 (43%), Gaps = 21/293 (7%) pir|T14867 interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| interaptin [Dictyostelium discoideum] Length = 1738

1569.6 Best-BlastP=>>nrprot 62% Identities = 310/738 (42%), Positives = 456/738 (61%), Gaps = 24/738 (3%) ref|NP_796632.1| primosomal protein N' [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC58516.1| primosomal protein N' [Vibrio parahaemolyticus] Length = 734

157.2 Best-BlastP=>>nrprot 90% Identities = 886/1061 (83%), Positives = 973/1061 (91%) gbj|AAM00612.1| chemiosmotic efflux system protein A-like protein [Legionella pneumophila] Length = 1066

1570.4 Best-BlastP=>>nrprot 74% Identities = 612/1047 (58%), Positives = 788/1047 (75%), Gaps = 9/1047 (0%) ref|ZP_00034374.1| COG0841: Cation/multidrug efflux pump [Burkholderia fungorum] Length = 1098

1575.2 Best-BlastP=>>nrprot 50% Identities = 46/122 (37%), Positives = 71/122 (58%), Gaps = 7/122 (5%) ref|NP_925923.1| MarR family transcriptional regulatory protein [Gloeobacter violaceus] dbj|BAC90918.1| MarR family transcriptional regulatory protein [Gloeobacter violaceus] Length = 143

1577.5 Best-BlastP=>>nrprot 63% Identities = 425/983 (43%), Positives = 617/983 (62%), Gaps = 35/983 (3%) ref|NP_288121.1| putative oxidase [Escherichia coli O157:H7 EDL933] ref|NP_310421.1| putative oxidase [Escherichia coli O157:H7 pir|B90928 probable oxidase [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|F85776 probable oxidase ydiJ [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gbj|AG56674.1|AE005391_11 putative oxidase [Escherichia coli O157:H7 EDL933] dbj|BAB35817.1| putative oxidase [Escherichia coli O157:H7] Length = 1018

1578.3 Best-BlastP=>>nrprot 67% Identities = 135/246 (54%), Positives = 173/246 (70%), Gaps = 3/246 (1%) ref|NP_436290.1| Hypothetical protein [Sinorhizobium meliloti] pir|D95392 protein [imported] - Sinorhizobium meliloti (strain 1021) Length = 408

1579.4 Best-BlastP=>>nrprot 44% Identities = 36/124 (29%), Positives = 68/124 (54%), Gaps = 5/124 (4%) ref|NP_635420.1| conserved hypothetical protein [Xanthomonas campestris] campestris str. ATCC 33913] gbj|AAM39344.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 143

158.2 Best-BlastP=>>nrprot 74% Identities = 139/205 (67%), Positives = 165/205 (80%), Gaps = 1/205 (0%) ref|NP_478237.1| ORF_ID:all7590~unknown protein [Nostoc sp. PCC 7120] pir|AC2538 hypothetical protein all7590 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120beta dbj|BAB77233.1| ORF_ID:all7590~unknown protein [Nostoc sp. PCC 7120] Length = 217

1581.4 Best-BlastP=>>nrprot No Hits found

1582.2 Best-BlastP=>>nrprot 76% Identities = 99/138 (71%), Positives = 115/138 (83%), Gaps = 2/138 (1%) ref|NP_233004.1| peptide methionine sulfoxide reductase [Vibrio cholerae O1 biovar Eltor str. N16961] pir|C82439 peptide methionine sulfoxide reductase VCA0615 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gbj|AAF96516.1| peptide methionine sulfoxide reductase [Vibrio cholerae O1 biovar Eltor str. N16961] Length = 394

1584.3 Best-BlastP=>>nrprot 79% Identities = 574/901 (63%), Positives = 711/901 (78%), Gaps = 7/901 (0%) ref|NP_285794.1| preprotein translocase; secretion protein [Escherichia coli O157:H7 EDL933] ref|NP_308129.1| preprotein translocase SecA [Escherichia coli O157:H7] ref|NP_752070.1| Preprotein translocase secA subunit [Escherichia coli CFT073] pir|F90641 preprotein translocase SecA [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|F85492 preprotein translocase, secretion protein [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gbj|AG54402.1|AE005186_8 preprotein translocase; secretion protein [Escherichia coli O157:H7 EDL933] dbj|BAB33525.1| preprotein translocase SecA [Escherichia coli O157:H7] gbj|AAN78614.1|AE016755_114 Preprotein translocase secA subunit [Escherichia coli CFT073] Length = 901

1585.2 Best-BlastP=>>nrprot 54% Identities = 115/350 (32%), Positives = 194/350 (55%), Gaps = 31/350 (8%) ref|NP_642273.1| flagellar protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM36809.1| flagellar protein [Xanthomonas axonopodis pv. citri str. 306] Length = 337

1586.2 Best-BlastP=>>nrprot No Hits found

1587.4 Best-BlastP=>>nrprot 43% Identities = 139/387 (35%), Positives = 203/387 (52%), Gaps = 19/387 (4%) ref|NP_643897.1| oxidoreductase [Xanthomonas axonopodis pv. citri str. 306] gb|AAM38433.1| oxidoreductase [Xanthomonas axonopodis pv. citri str. 306] Length = 443

1589.3 Best-BlastP=>>nrprot 79% Identities = 138/220 (62%), Positives = 179/220 (81%), Gaps = 2/220 (0%) ref|NP_820222.1| DNA-binding response regulator [Coxiella burnetii RSA 493] gb|AAO90736.1| DNA-binding response regulator [Coxiella burnetii RSA 493] Length = 223

159.1 Best-BlastP=>>nrprot 54% Identities = 44/97 (45%), Positives = 57/97 (58%), Gaps = 14/97 (14%) ref|NP_747491.1| hypothetical protein [Pseudomonas putida KT2440] gb|AAN70955.1|AE016739_8 hypothetical protein [Pseudomonas putida KT2440] Length = 91

1590.1 Best-BlastP=>>nrprot 69% Identities = 92/172 (53%), Positives = 126/172 (73%) ref|NP_819923.1| intracellular septation protein A [Coxiella burnetii RSA 493] gb|AAC90437.1| intracellular septation protein A [Coxiella burnetii RSA 493] Length = 181

1591.4 Best-BlastP=>>nrprot 56% Identities = 183/441 (41%), Positives = 275/441 (62%), Gaps = 13/441 (2%) ref|ZP_00065233.1| COG0741: Soluble regulatory proteins (some contain LysM/invasin domains) [Microbulbifer degradans 2-40] Length = 543

1592.3 Best-BlastP=>>nrprot 62% Identities = 130/295 (44%), Positives = 191/295 (64%) ref|NP_406039.1| putative membrane protein [Yersinia pestis] ref|NP_669001.1| hypothetical [Yersinia pestis KIM] pir|AB0306 probable membrane protein YPO2505 [imported] - Yersinia pestis (strain CO92) emb|CAC91310.1| putative membrane protein [Yersinia pestis CO92] gb|AAM85252.1|AE013771_7 hypothetical [Yersinia pestis KIM] Length = 312

1594.2 Best-BlastP=>>nrprot 57% Identities = 83/248 (33%), Positives = 138/248 (55%), Gaps = 14/248 (5%) ref|NP_842295.1| possible BioH, catalyzes some early step in biotin biosynthesis [Nitrosomonas europaea ATCC 19718] emb|CAD86210.1| possible BioH, catalyzes some early step in biotin biosynthesis

1595.3 Best-BlastP=>>nrprot 52% Identities = 130/329 (39%), Positives = 199/329 (60%), Gaps = 2/329 (0%) ref|NP_790344.1| 8-amino-7-oxononanoate synthase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54039.1| 8-amino-7-oxononanoate synthase [Pseudomonas syringae pv. tomato str. DC3000] Length = 396

1598.6 Best-BlastP=>>nrprot 75% Identities = 189/307 (61%), Positives = 240/307 (78%) gb|AAG47791.1|AF311738_7 BioB [Mesorhizobium loti] emb|CAD31399.1| BIOTIN SYNTHASE PROTEIN [Mesorhizobium loti] Length = 331

1599.4 Best-BlastP=>>nrprot 48% Identities = 481/1746 (27%), Positives = 836/1746 (47%), Gaps = 149/1746 (8%) ref|NP_932226.1| putative conjugative transfer protein Tral [Vibrio vulnificus YJ016] dbj|BAC97749.1| putative conjugative transfer protein Tral [Vibrio vulnificus YJ016] Length = 1924

16.1 Best-BlastP=>>nrprot 60% Identities = 34/55 (61%), Positives = 42/55 (76%) ref|NP_890077.1| putative phage excisionase [Bordetella bronchiseptica] emb|CAE34036.1| putative phage excisionase [Bordetella bronchiseptica] Length = 84

160.1 Best-BlastP=> >nrprot 35% Identities = 36/95 (37%), Positives = 43/95 (45%), Gaps = 7/95 (7%) gb|AAF86199.1|AF2388885_2 VrrB [Bacillus anthracis] Length = 265

1601.3 Best-BlastP=> >nrprot 61% Identities = 166/370 (44%), Positives = 236/370 (63%), Gaps = 17/370 (4%) ref|NP_660996.1| glycosyl hydrolase, family 3 [Chlorobium tepidum TLS] gb|AAM71338.1| glycosyl hydrolase, family 3 [Chlorobium tepidum TLS] Length = 372

1602.2 Best-BlastP=> >nrprot 52% Identities = 133/394 (33%), Positives = 207/394 (52%), Gaps = 17/394 (4%) ref|NP_798008.1| putative SAM-dependent methyltransferase [Vibrio parahaemolyticus] RIMD 2210633] dbj|BAC59892.1| putative SAM-dependent methyltransferase [Vibrio parahaemolyticus] Length = 418

1603.3 Best-BlastP=> >nrprot 10% Identities = 40/105 (38%), Positives = 55/105 (52%), Gaps = 5/105 (4%) pdb|1N0R|A Chain A, 4ank: A Designed Ankyrin Repeat Protein With Four Identical Consensus Repeats Length = 126

1606.2 Best-BlastP=> >nrprot 64% Identities = 136/270 (50%), Positives = 178/270 (65%) ref|ZP_00065849.1| COG0266: Formamidopyrimidine-DNA glycosylase [Microbulbifer degradans 2-40] Length = 271

1607.2 Best-BlastP=> >nrprot 55% Identities = 24/78 (30%), Positives = 43/78 (55%), Gaps = 1/78 (1%) ref|NP_820114.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90628.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 105

1608.2 Best-BlastP=> >nrprot 70% Identities = 201/383 (52%), Positives = 279/383 (72%) ref|NP_903067.1| probable stearoyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] gb|AAQ61061.1| probable stearoyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] Length = 405

1611.5 Best-BlastP=> >nrprot 75% Identities = 206/338 (60%), Positives = 260/338 (76%), Gaps = 1/338 (0%) ref|ZP_00085994.1| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase [Pseudomonas fluorescens PRO-1] Length = 679

1615.2 Best-BlastP=> >nrprot 64% Identities = 291/607 (47%), Positives = 389/607 (64%), Gaps = 17/607 (2%) ref|NP_826054.1| putative oxidoreductase [Streptomyces avermitilis MA-4680] dbj|BAC72589.1| putative oxidoreductase [Streptomyces avermitilis MA-4680] Length = 642

1617.3 Best-BlastP=> >nrprot 62% Identities = 77/167 (46%), Positives = 107/167 (64%), Gaps = 3/167 (1%) ref|NP_820461.1| alkylhydroperoxidase AhpD family core domain protein [Coxiella burnetii RSA 493] Length = 177

1618.3 Best-BlastP=> >nrprot 97% Identities = 159/162 (98%) spl|P53637|SODC_LEGPN Superoxide dismutase [Cu-Zn] precursor dbj|BAA06223.1| [Cu,Zn]-superoxide dismutase [Legionella pneumophila] gb|AAB36467.1| periplasmic copper-zinc superoxide dismutas; CuZnSOD [Legionella pneumophila] Length = 162

1623.4 Best-BlastP=> >nrprot 46% Identities = 115/438 (26%), Positives = 202/438 (46%), Gaps = 28/438 (6%) ref|NP_873416.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] gb|AAP95805.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] Length = 665

1624.4 Best-BlastP=> >nrprot 42% Identities = 121/543 (22%), Positives = 225/543 (41%), Gaps = 73/543 (13%) ref|ZP_00089633.1| hypothetical protein [Azotobacter vinelandii] Length = 642

1625.3 Best-BlastP=> >nrprot 90% Identities = 317/379 (83%), Positives = 345/379 (91%) gb|AAP88975.1| S-adenosylmethionine synthetase [Amoeba proteus symbiotic bacterium] Length = 381

1626.3 Best-BlastP=>>nrprot 83% Identities = 321/427 (75%), Positives = 368/427 (86%) ref|NP_821004.1| adenosylhomocysteinase [Coxiella burnetii RSA 493] gb|AAO91518.1| adenosylhomocysteinase [Coxiella burnetii RSA 493] Length = 429

1628.3 Best-BlastP=>>nrprot 56% Identities = 118/268 (44%), Positives = 154/268 (57%), Gaps = 21/268 (7%) ref|NP_771454.1| bli4814 [Bradyrhizobium japonicum] dbj|BAC50079.1| bli4814 [Bradyrhizobium japonicum USDA 110] Length = 262

1629.1 Best-BlastP=>>nrprot 54% Identities = 88/251 (35%), Positives = 138/251 (54%), Gaps = 19/251 (7%) ref|NP_771455.1| bli4815 [Bradyrhizobium japonicum] dbj|BAC50080.1| bli4815 [Bradyrhizobium japonicum USDA 110] Length = 235

163.1 Best-BlastP=>>nrprot 74% Identities = 237/426 (55%), Positives = 324/426 (76%) ref|ZP_00072043.1| COG0334: Glutamate dehydrogenase/leucine dehydrogenase [Trichodesmium erythraeum IMS101] Length = 428

1631.3 Best-BlastP=>>nrprot 60% Identities = 264/625 (42%), Positives = 366/625 (58%), Gaps = 65/625 (10%) ref|NP_771456.1| bli4816 [Bradyrhizobium japonicum] dbj|BAC50081.1| bli4816 [Bradyrhizobium japonicum USDA 110] Length = 649

1632.3 Best-BlastP=>>nrprot 69% Identities = 276/567 (48%), Positives = 411/567 (72%), Gaps = 4/567 (0%) ref|NP_819875.1| ABC transporter, ATP-binding/permease protein [Coxiella burnetii RSA 493] gb|AAO90389.1| ABC transporter, ATP-binding/permease protein [Coxiella burnetii RSA 493] Length = 589

1633.2 Best-BlastP=>>nrprot 63% Identities = 142/305 (46%), Positives = 203/305 (66%), Gaps = 11/305 (3%) ref|NP_438232.1| tetraacylydisaccharide 4'-kinase-like protein [Haemophilus influenzae Rd] sp|P44491|LPXK_HAEIN Tetraacylydisaccharide 4'-kinase (Lipid A 4'-kinase) pir|G64141 probable tetraacylydisaccharide 4'-kinase (EC 2.7.1.130) HI0059 [similarity] - Haemophilus influenzae (strain Rd KW20) gb|AAC21737.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 332

1635.4 Best-BlastP=>>nrprot 16% Identities = 86/371 (23%), Positives = 164/371 (44%), Gaps = 39/371 (10%) pir|T24806 hypothetical protein T10G3.5 - Caenorhabditis elegans Length = 1164

1636.2 Best-BlastP=>>nrprot 73% Identities = 660/1159 (56%), Positives = 841/1159 (72%), Gaps = 16/1159 (1%) ref|NP_454838.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_804113.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica subsp. enterica serovar Typhi (strain CT18) emb|CAD08689.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO67962.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 1160

1638.2 Best-BlastP=>>nrprot 76% Identities = 256/395 (64%), Positives = 304/395 (76%), Gaps = 3/395 (0%) ref|NP_642338.1| 3-ketoacyl-CoA thiolase [Xanthomonas axonopodis pv. citri str. 306] gb|AAM36874.1| 3-ketoacyl-CoA thiolase [Xanthomonas axonopodis pv. citri str. 306] Length = 401

1639.4 Best-BlastP=>>nrprot No Hits found

1641.5 Best-BlastP=>>nrprot 63% Identities = 190/434 (43%), Positives = 282/434 (64%), Gaps = 5/434 (1%) ref|NP_793501.1| trigger factor [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57196.1| trigger factor [Pseudomonas syringae pv. tomato str. DC3000] Length = 436

1642.3 Best-BlastP=>>nrprot 82% Identities = 150/203 (73%), Positives = 178/203 (87%), Gaps = 1/203 (0%) ref|NP_455045.1| ATP-dependent clip protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_459444.1| proteolytic subunit of clipA-clipP ATP-dependent serine protease, heat shock protein F21.5 [Salmonella typhimurium LT2] ref|NP_806142.1| ATP-dependent clip protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi Ty2] sp|Q9LC07|CLPP_SALTY ATP-dependent Clip protease proteolytic subunit [Endopeptidase Clip] pir|AC0558 ATP-dependent clip protease proteolytic chain [imported] - *Salmonella enterica* subsp. *enterica* serovar *Typhi* (strain CT18) dbj|BA94668.1| serine protease subunit [Salmonella typhimurium] gb|AAL19403.1| proteolytic subunit of clipA-clipP ATP-dependent serine protease [Salmonella typhimurium LT2] emb|CADD08907.1| ATP-dependent clip protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO70002.1| ATP-dependent clip protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi Ty2]
Length = 207

1643.4 Best-BlastP=>>nrprot 97% Identities = 791/816 (96%), Positives = 800/816 (98%) gb|AAM00615.1| response regulator *TutC*-like protein [Legionella pneumophila]
Length = 816

1644.6 Best-BlastP=>>nrprot 59% Identities = 171/417 (41%), Positives = 246/417 (58%), Gaps = 9/417 (2%) ref|NP_772134.1| bli5494 [Bradyrhizobium japonicum] dbj|BAC50759.1| bli5494 [Bradyrhizobium japonicum USDA 110]
Length = 415

1645.1 Best-BlastP=>>nrprot 59% Identities = 76/172 (44%), Positives = 110/172 (63%) ref|NP_717325.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN54769.1|AE015617_4 conserved hypothetical protein [Shewanella oneidensis MR-1]
Length = 183

1647.2 Best-BlastP=>>nrprot 67% Identities = 101/180 (56%), Positives = 127/180 (70%), Gaps = 1/180 (0%) ref|NP_715765.1| acyltransferase family protein [Shewanella oneidensis MR-1] gb|AAN53210.1|AE015463_7 acyltransferase family protein [Shewanella oneidensis MR-1]
Length = 186

1649.3 Best-BlastP=>>nrprot 53% Identities = 276/732 (37%), Positives = 397/732 (54%), Gaps = 63/732 (8%) ref|NP_832882.1| hypothetical protein [Bacillus cereus ATCC 14579] gb|AAP10083.1| hypothetical protein [Bacillus cereus ATCC 14579]
Length = 854

1650.2 Best-BlastP=>>nrprot 35% Identities = 119/317 (37%), Positives = 181/317 (57%), Gaps = 6/317 (1%) ref|NP_832883.1| NADH-quinone oxidoreductase chain L [Bacillus cereus ATCC 14579] gb|AAP10084.1| NADH-quinone oxidoreductase chain L [Bacillus cereus ATCC 14579]
Length = 510

1652.4 Best-BlastP=>>nrprot 35% Identities = 37/135 (27%), Positives = 67/135 (49%), Gaps = 11/135 (8%) pir|I40884 cytotoxin L - Clostridium sordelli emb|CAAA57959.1| cytotoxin L [Clostridium sordelli]
Length = 2364

1653.3 Best-BlastP=>>nrprot 63% Identities = 142/281 (50%), Positives = 195/281 (69%), Gaps = 1/281 (0%) pir|A42928 plasminogen activator precursor - *Yersinia pestis*
Length = 312

1655.2 Best-BlastP=>>nrprot 81% Identities = 41/60 (68%), Positives = 49/60 (81%), Gaps = 2/60 (3%) ref|NP_842168.1| Tetraacyldisaccharide-1-P 4'-kinase [Nitrosomonas europaea ATCC 19718] emb|CAD86075.1| Tetraacyldisaccharide-1-P 4'-kinase [Nitrosomonas europaea ATCC 19718]
Length = 396

1657.1 Best-BlastP=>>nrprot 64% Identities = 124/250 (49%), Positives = 163/250 (65%), Gaps = 7/250 (2%) ref|NP_872922.1| 3-deoxy-manno-oculosonate cytidylyltransferase [Haemophilus ducreyi 35000HP]
[Haemophilus ducreyi 35000HP]
Length = 253

1658.2 Best-BlastP=>>nrprot 33% Identities = 96/392 (24%), Positives = 148/392 (37%), Gaps = 116/392 (29%) ref|ZP_00067367.1| COG2730:
Endoglucanase [Microbulbifer degradans 2-40]
Length = 725

1659.4 Best-BlastP=>>nrprot 25% Identities = 156/726 (21%), Positives = 334/726 (46%), Gaps = 107/726 (14%) pir|A47297 myosin heavy chain form B, nonmuscle - African clawed frog gb|AAA49915.1| nonmuscle myosin heavy chain b Length = 1992

166.2 Best-BlastP=>>nrprot 96% Identities = 1010/1064 (94%), Positives = 1030/1064 (96%), Gaps = 4/1064 (0%) gb|AAM00617.1| putative copper efflux ATPase [Legionella pneumophila] Length = 1060

1660.2 Best-BlastP=>>nrprot No Hits found

1661.3 Best-BlastP=>>nrprot 61% Identities = 110/213 (51%), Positives = 140/213 (65%), Gaps = 1/213 (0%) sp|Q8DDY0|RADC_VIBVU DNA repair protein radC homolog dbj|BAC93049.1| DNA repair protein [Vibrio vulnificus YJ016] Length = 224

1663.6 Best-BlastP=>>nrprot 86% Identities = 1036/1406 (73%), Positives = 1216/1406 (86%), Gaps = 14/1406 (0%) ref|NP_742614.1| DNA-directed RNA polymerase, beta' subunit [Pseudomonas putida KT2440] gb|AAN66078.1|AE016237_2 DNA-directed RNA polymerase, beta'

1664.2 Best-BlastP=>>nrprot 29% Identities = 47/193 (24%), Positives = 80/193 (41%), Gaps = 13/193 (6%) ref|ZP_00046942.1| COG3064: Membrane protein involved in colicin uptake [Lactobacillus gasseri] Length = 962

1666.3 Best-BlastP=>>nrprot No Hits found

1669.3 Best-BlastP=>>nrprot 68% Identities = 177/313 (56%), Positives = 220/313 (70%) ref|NP_617527.1| triacylglycerol lipase [Methanotosarcina acetivorans str. C2A] Length = 321

1670.3 Best-BlastP=>>nrprot 16% Identities = 43/147 (29%), Positives = 74/147 (50%), Gaps = 6/147 (4%) ref|XP_323831.1| predicted protein [Neurospora crassa] gb|EAA27811.1| predicted protein [Neurospora crassa] Length = 554

1671.3 Best-BlastP=>>nrprot No Hits found

1673.5 Best-BlastP=>>nrprot 31% Identities = 97/388 (25%), Positives = 174/388 (44%), Gaps = 42/388 (10%) pir|F86291 hypothetical protein F7H2.8 [Imported] - Arabidopsis thaliana gb|AAF82144.1|AC034256_8 Contains similarity to F-box protein FBL2 from Homo sapiens gb|AF176518 and contains multiple Leucine Rich PF|00560 repeats. ESTs gb|Z34572, gb|Z34571, gb|AI100681, gb|AI100675, gb|AA395320, gb|AI100674, gb|AA651378, gb|AA007067, gb|T22090, gb|AI995016, gb|H36884, gb|AI995066, gb|H37061, gb|T43537 come from this gene. [Arabidopsis thaliana] Length = 568

1675.3 Best-BlastP=>>nrprot 39% Identities = 20/67 (29%), Positives = 42/67 (62%) ref|NP_439878.1| hypothetical protein [Haemophilus influenzae Rd] sp|P44300|YH36_HAEIN Hypothetical protein H11736 pir|D64041 hypothetical protein H11736 - Haemophilus influenzae (strain Rd KW20) gb|AAC23384.1| H. influenzae predicted coding region H11736 [Haemophilus influenzae Rd] Length = 77

168.1 Best-BlastP=>>nrprot 42% Identities = 43/160 (26%), Positives = 75/160 (46%), Gaps = 25/160 (15%) ref|NP_437473.1| hypothetical membrane protein [Sinorhizobium meliloti] pir|E95958 hypothetical membrane protein [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb|CAC49333.1| hypothetical membrane protein [Sinorhizobium meliloti] Length = 172

1681.5 Best-BlastP=>>nrprot 65% Identities = 432/984 (43%), Positives = 629/984 (63%), Gaps = 47/984 (4%) ref|NP_927961.1| RNA polymerase associated protein (ATP-dependent helicase) [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE12910.1| RNA polymerase associated protein (ATP-dependent helicase) [Photorhabdus luminescens subsp. laumontii TTO1] Length = 970

1682.4 Best-BlastP=>>nrprot 35% Identities = 63/190 (33%), Positives = 105/190 (55%), Gaps = 8/190 (4%) ref|ZP_00065413.1| COG3000: Sterol desaturase [Microbulbifer degradans 2-40] Length = 273

1683.2 Best-BlastP=>>nrprot No Hits found

1684.3 Best-BlastP=>>nrprot No Hits found

1685.3 Best-BlastP=>>nrprot 72% Identities = 199/372 (53%), Positives = 270/372 (72%), Gaps = 3/372 (0%) ref|ZP_00016064.1| COG0842: ABC-type multidrug transport system, permease component [Rhodospirillum rubrum] Length = 376

1689.3 Best-BlastP=>>nrprot 68% Identities = 207/377 (54%), Positives = 275/377 (72%), Gaps = 9/377 (2%) ref|NP_720122.1| cytochrome c oxidase, subunit II [Shewanella oneidensis MR-1] gb|AAN57566.1|AE015892_6 cytochrome c oxidase, subunit II [Shewanella oneidensis MR-1] Length = 513

169.1 Best-BlastP=>>nrprot 86% Identities = 55/68 (80%), Positives = 60/68 (88%) gb|AAM00618.1| unknown [Legionella pneumophila] Length = 68

1691.3 Best-BlastP=>>nrprot 84% Identities = 388/528 (73%), Positives = 458/528 (86%), Gaps = 8/528 (1%) ref|NP_720123.1| cytochrome c oxidase, subunit I [Shewanella oneidensis MR-1] gb|AAN57567.1|AE015892_7 cytochrome c oxidase, subunit I [Shewanella oneidensis MR-1] Length = 530

1692.2 Best-BlastP=>>nrprot 86% Identities = 473/671 (70%), Positives = 577/671 (85%), Gaps = 7/671 (1%) ref|NP_819550.1| exoribnuclease ABC, B subunit [Coxiella burnetii RSA 493] gb|AAO909064.1| exoribnuclease ABC, B subunit [Coxiella burnetii RSA 493] Length = 672

1693.2 Best-BlastP=>>nrprot 56% Identities = 2775 (36%), Positives = 4575 (60%) ref|NP_754358.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN80925.1|AE016762_178 Hypothetical protein [Escherichia coli CFT073] Length = 82

1692.2 Best-BlastP=>>nrprot 56% Identities = 118/355 (33%), Positives = 189/355 (53%), Gaps = 47/355 (13%) ref|NP_884030.1| conserved hypothetical protein [Bordetella parapertussis] emb|CAE37058.1| conserved hypothetical protein [Bordetella parapertussis] Length = 392

1697.2 Best-BlastP=>>nrprot 56% Identities = 66/174 (37%), Positives = 104/174 (59%), Gaps = 2/174 (1%) ref|ZP_00013244.1| COG3038: Cytochrome B561 [Rhodospirillum rubrum] Length = 188

1698.2 Best-BlastP=>>nrprot 35% Identities = 84/273 (30%), Positives = 130/273 (47%), Gaps = 17/273 (6%) ref|ZP_000085491.1| COG0354: Predicted aminomethyltransferase related to GcvT [Pseudomonas fluorescens PfO-1] Length = 313

1699.4 Best-BlastP=>>nrprot 58% Identities = 130/277 (46%), Positives = 176/277 (63%), Gaps = 6/277 (2%) ref|ZP_00090118.1| COG0771: UDP-N-acetylglucosamine-D-glutamate ligase [Azotobacter vinelandii] Length = 448

1701.5 Best-BlastP=>>nrprot 66% Identities = 192/359 (53%), Positives = 262/359 (72%) ref|NP_819182.1| cell division protein FtsW [Coxiella burnetii RSA 493] gb|AAD39750.1|AF123260_1 FtsW [Coxiella burnetii] gb|AAO89696.1| cell division protein FtsW [Coxiella burnetii RSA 493] Length = 372

1703.1 Best-BlastP=>>nrprot 36% Identities = 57/215 (26%), Positives = 93/215 (43%), Gaps = 32/215 (14%) ref|NP_780971.1| DNA helicase [Clostridium tetani E88] gb|AAO34908.1| DNA helicase [Clostridium tetani E88] Length = 1352

1704.4 Best-BlastP=>>nrprot 8% Identities = 33/108 (30%), Positives = 55/108 (50%), Gaps = 5/108 (4%) ref|NP_266277.1| hypothetical protein [Lactococcus lactis subsp. lactis] pirl|A86640 hypothetical protein ybcH [imported] - Lactococcus lactis subsp. lactis (strain IL1403) Length = 311

1705.2 Best-BlastP=>>nrprot No Hits found

1706.2 Best-BlastP=> >nrprot 56% Identities = 62/148 (41%), Positives = 86/148 (58%), Gaps = 7/148 (4%) ref|ZP_00054547.1| COG0350: Methylated DNA-protein cysteine methyltransferase [Magnetospirillum magnetotacticum] Length = 183

1707.2 Best-BlastP=> >nrprot 85% Identities = 96/117 (82%), Positives = 104/117 (88%), Gaps = 2/117 (1%) ref|ZP_00091602.1| COG0335: Ribosomal protein L19 [Azotobacter vinelandii] Length = 116

1708.4 Best-BlastP=> >nrprot 52% Identities = 44/123 (35%), Positives = 65/123 (52%), Gaps = 6/123 (4%) ref|ZP_00134742.1| COG3109: Activator of osmoprotectant transporter ProP [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 182

1709.1 Best-BlastP=> >nrprot 65% Identities = 114/228 (50%), Positives = 152/228 (66%), Gaps = 2/228 (0%) ref|NP_819391.1| 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493] gb|AAO89905.1| 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493]

1711.2 Best-BlastP=> >nrprot 36% Identities = 49/177 (27%), Positives = 88/177 (49%), Gaps = 15/177 (8%) gb|EAA36774.1| GLP_193_16037_16813 [Giardia lamblia ATCC 50803] Length = 258

1713.2 Best-BlastP=> >nrprot 64% Identities = 314/686 (45%), Positives = 445/686 (64%), Gaps = 3/686 (0%) ref|NP_820891.1| glycyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] sp|P45651|SYGB_COXBU Glycyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] (GlyRS) gb|AAO91405.1| glycyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] Length = 689

1714.4 Best-BlastP=> >nrprot 85% Identities = 224/291 (76%), Positives = 258/291 (88%) ref|NP_820890.1| glycyl-tRNA synthetase, alpha subunit [Coxiella burnetii RSA 493] sp|P94616|SYGA_COXBU Glycyl-tRNA synthetase alpha chain (Glycine-tRNA ligase alpha chain) (GlyRS) em|CAA71456.1| unnamed protein product [Coxiella burnetii] gb|AAO91404.1| glycyl-tRNA synthetase, alpha subunit [Coxiella burnetii RSA 493] Length = 319

172.1 Best-BlastP=> >nrprot 69% Identities = 28/58 (48%), Positives = 44/58 (75%) ref|ZP_00053249.1| hypothetical protein [Magnetospirillum magnetotacticum] ref|ZP_00101210.1| hypothetical protein [Desulfobacterium hafniense] Length = 60

1720.3 Best-BlastP=> >nrprot 24% Identities = 37/126 (29%), Positives = 64/126 (50%), Gaps = 3/126 (2%) ref|NP_371995.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus Mu50] ref|NP_374585.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus N315] ref|NP_646177.1| menaquinone biosynthesis methyltransferase [imported] - Staphylococcus subsp. aureus subsp. aureus N315] dbj|BAB42564.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus Mu50] dbj|BAB95225.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus MuV2] Length = 241

1722.2 Best-BlastP=> >nrprot 55% Identities = 123/307 (40%), Positives = 173/307 (56%), Gaps = 9/307 (2%) ref|NP_781246.1| glutaminase [Clostridium tetani E88] gb|AAO35183.1| glutaminase [Clostridium tetani E88] Length = 306

1723.5 Best-BlastP=> >nrprot 59% Identities = 71/181 (39%), Positives = 111/181 (61%), Gaps = 9/181 (4%) ref|NP_346734.1| D-3 phosphoglycerate dehydrogenase [Clostridium acetobutylicum] pir|G96910 D-3 phosphoglycerate dehydrogenase [imported] - Clostridium acetobutylicum gb|AAK78074.1|AE007521_8 D-3 phosphoglycerate dehydrogenase [Clostridium acetobutylicum] Length = 318

1724.3 Best-BlastP=>>nrprot 35% Identities = 62/241 (25%), Positives = 104/241 (43%), Gaps = 20/241 (8%) ref|NP_102317.1| probable hydrolase [Mesorhizobium loti] dbj|BAB48103.1| probable hydrolase [Mesorhizobium loti] Length = 248

1725.3 Best-BlastP=>>nrprot 74% Identities = 172/279 (61%), Positives = 212/279 (75%) ref|NP_747209.1| RNA polymerase sigma-32 factor [Pseudomonas putida KT2440] gb|AAF80334.1|AF157048_1 heat shock sigma factor RpoH [Pseudomonas putida] gb|AAN70673.1|AE016711_1 RNA polymerase sigma-32 factor [Pseudomonas putida KT2440] Length = 284

1726.4 Best-BlastP=>>nrprot 14% Identities = 50/174 (28%), Positives = 82/174 (47%), Gaps = 18/174 (10%) ref|NP_473239.1| hypothetical protein [Plasmidium falciparum 3D7] pirl|T18459 hypothetical protein C0515c - malaria parasite (Plasmidium falciparum) emb|CAA15601.1| hypothetical protein [Plasmidium falciparum 3D7] Length = 1236

1727.3 Best-BlastP=>>nrprot 72% Identities = 498/899 (55%), Positives = 632/899 (70%), Gaps = 39/899 (4%) ref|NP_668025.1| protein chain initiation factor IF-2 [Yersinia pestis KIM] sp|Q8ZBC2|IF2_YERPE Translation initiation factor IF-2 gb|AAP84276.1|AE013671_3 protein chain initiation factor IF-2 [Yersinia pestis KIM] Length = 892

1728.3 Best-BlastP=>>nrprot 70% Identities = 225/399 (56%), Positives = 293/399 (73%), Gaps = 1/399 (0%) ref|NP_653663.1| SDF, Sodium:dicarboxylate symporter family [Bacillus anthracis A2012] ref|NP_847618.1| proton/glutamate symporter family protein, putative [Bacillus anthracis str. Ames] Length = 405

1729.2 Best-BlastP=>>nrprot No Hits found

1730.3 Best-BlastP=>>nrprot 34% Identities = 88/258 (34%), Positives = 129/258 (50%), Gaps = 30/258 (11%) ref|NP_052868.1| hypothetical protein [Coxiella burnetii] gb|AAD33500.1|AF131076_26 hypothetical protein [Coxiella burnetii] Length = 361

1731.3 Best-BlastP=>>nrprot 84% Identities = 284/394 (72%), Positives = 339/394 (86%) ref|ZP_00065178.1| COG0133: Tryptophan synthase beta chain [Microbulbifer degradans 2-40] Length = 403

1732.2 Best-BlastP=>>nrprot 65% Identities = 95/197 (48%), Positives = 136/197 (69%) ref|NP_902433.1| phosphoribosylanthranilate isomerase [Chromobacterium violaceum ATCC 12472] gb|AAQ60431.1| phosphoribosylanthranilate isomerase [Chromobacterium violaceum ATCC 12472] Length = 206

1734.1 Best-BlastP=>>nrprot 71% Identities = 165/284 (58%), Positives = 206/284 (72%) ref|NP_820298.1| peptide methionine sulfoxide reductase [Coxiella burnetii RSA 493] gb|AAO90812.1| peptide methionine sulfoxide reductase [Coxiella burnetii RSA 493] Length = 284

1735.3 Best-BlastP=>>nrprot 73% Identities = 148/259 (57%), Positives = 193/259 (74%), Gaps = 1/259 (0%) ref|ZP_00087161.1| COG0101: Pseudouridylate synthase [Pseudomonas fluorescens PFO-1] Length = 313

1736.3 Best-BlastP=>>nrprot 79% Identities = 163/239 (68%), Positives = 198/239 (82%), Gaps = 1/239 (0%) ref|ZP_00091549.1| COG0528: Uridylate kinase [Azotobacter vinelandii] Length = 249

1737.4 Best-BlastP=>>nrprot 84% Identities = 118/184 (64%), Positives = 158/184 (85%) ref|NP_928020.1| ribosome releasing factor [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE12970.1| ribosome releasing factor [Photorhabdus luminescens subsp. laumontii TTO1] Length = 185

1746.2 Best-BlastP=>>nrprot 47% Identities = 71/209 (33%), Positives = 100/209 (47%), Gaps = 8/209 (3%) ref|NP_233145.1| arginine ABC transporter, periplasmic arginine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|H82420 arginine ABC transporter, periplasmic arginine-binding protein VCA0759 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1) gb|AAF96657.1| arginine ABC transporter, periplasmic arginine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 243

1747.2 Best-BlastP=>>nrprot No Hits found

1748.3 Best-BlastP=>>nrprot 57% Identities = 160/430 (37%), Positives = 244/430 (56%), Gaps = 14/430 (3%) ref|NP_662910.1| threonine synthase [Chlorobium tepidum TLS] gb|AAM73252.1| threonine synthase [Chlorobium tepidum TLS] Length = 441

1749.2 Best-BlastP=>>nrprot 29% Identities = 48/192 (25%), Positives = 77/192 (40%), Gaps = 21/192 (10%) ref|NP_698612.1| outer membrane protein, 31 kDa [Brucella suis 1330] gb|AAN30527.1|AE014455_11 outer membrane protein, 31 kDa [Brucella suis 1330] Length = 261

1750.3 Best-BlastP=>>nrprot 69% Identities = 162/295 (54%), Positives = 201/295 (68%), Gaps = 6/295 (2%) ref|NP_742276.1| cytochrome c oxidase, subunit III [Pseudomonas putida KT2440] gb|AAN65740.1|AE016200_4 cytochrome c oxidase, subunit III [Pseudomonas putida KT2440] Length = 295

1752.2 Best-BlastP=>>nrprot 66% Identities = 83/173 (47%), Positives = 120/173 (69%), Gaps = 2/173 (1%) ref|NP_720124.1| cytochrome c oxidase assembly protein coxG [Shewanella oneidensis MR-1] gb|AAN57568.1|AE015892_8 cytochrome c oxidase assembly protein coxG [Shewanella oneidensis MR-1] Length = 193

1754.3 Best-BlastP=>>nrprot 49% Identities = 174/422 (41%), Positives = 252/422 (59%), Gaps = 9/422 (2%) ref|NP_820704.1| thiol:disulfide interchange protein DsbD [Coxiella burnetii RSA 493] gb|AO91218.1| thiol:disulfide interchange protein DsbD [Coxiella burnetii RSA 493] Length = 584

1755.3 Best-BlastP=>>nrprot No Hits found

1756.4 Best-BlastP=>>nrprot 63% Identities = 133/271 (49%), Positives = 181/271 (66%) ref|NP_902359.1| probable oxidoreductase, short-chain dehydrogenase/reductase family [Chromobacterium violaceum ATCC 12472] gb|AAQ60359.1| probable oxidoreductase, short-chain dehydrogenase/reductase family [Chromobacterium violaceum ATCC 12472] Length = 278

1759.4 Best-BlastP=>>nrprot 43% Identities = 55/224 (24%), Positives = 102/224 (45%), Gaps = 3/224 (1%) ref|NP_746234.1| conserved hypothetical protein [Pseudomonas putida KT2440] gb|AAN69698.1|AE016606_1 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 267

176.1 Best-BlastP=>>nrprot No Hits found

1760.4 Best-BlastP=>>nrprot 75% Identities = 116/223 (52%), Positives = 170/223 (76%) ref|XP_306643.1| ENSANGP00000000843 [Anopheles gambiae] gb|EA02110.1| ENSANGP00000000843 [Anopheles gambiae str. PEST] Length = 228

1761.4 Best-BlastP=>>nrprot 9% Identities = 54/209 (25%), Positives = 100/209 (47%), Gaps = 38/209 (18%) ref|ZP_00010059.1| COG1680: Beta-lactamase class C and other penicillin binding proteins [Rhodopseudomonas palustris] Length = 395

1762.2 Best-BlastP=>>nrprot 39% Identities = 66/245 (26%), Positives = 125/245 (51%), Gaps = 9/245 (3%) ref|NP_834835.1| Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] gb|AAP12036.1| Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] Length = 254

1764.3 Best-BlastP=>>nrprot 99% Identities = 377/377 (100%), Positives = 377/377 (100%) emb|CAB6521.1| N-acylglucosamine 2-epimerase [Legionella pneumophila] Length = 377

1765.4 Best-BlastP=>>nrprot 99% Identities = 201/201 (100%), Positives = 201/201 (100%) emb|CAB65210.1| putative acetyl transferase [Legionella pneumophila] Length = 419

1767.2 Best-BlastP=>>nrprot 56% Identities = 103/234 (44%), Positives = 135/234 (57%), Gaps = 1/234 (0%) pf|1712315B glycerophosphoryl diester esterase Length = 247

1768.3 Best-BlastP=>>nrprot 52% Identities = 150/405 (37%), Positives = 216/405 (53%), Gaps = 12/405 (2%) ref|NP_519385.1| PROBABLE GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC LIPOPROTEIN SIGNAL PEPTIDE [Ralstonia solanacearum] emb|CAD14966.1| PROBABLE GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC LIPOPROTEIN SIGNAL PEPTIDE [Ralstonia solanacearum] Length = 438

1770.2 Best-BlastP=>>nrprot 99% Identities = 1034/1035 (99%), Positives = 1034/1035 (99%) gb|AAF32510.1|AF095231_1 defect in organelle trafficking protein [Legionella pneumophila] Length = 1035

1772.1 Best-BlastP=>>nrprot 94% Identities = 135/151 (89%), Positives = 144/151 (95%) gb|AAC35591.1| lcmV [Legionella pneumophila] Length = 151

1773.1 Best-BlastP=>>nrprot 99% Identities = 150/151 (99%), Positives = 151/151 (100%) pir|S61384 lcmW protein - Legionella pneumophila gb|AAC35589.1| lcmW [Legionella pneumophila] Length = 151

1774.2 Best-BlastP=>>nrprot 90% Identities = 411/472 (87%), Positives = 426/472 (90%), Gaps = 6/472 (1%) gb|AAC35590.1| lcmX [Legionella pneumophila] Length = 466

1775.3 Best-BlastP=>>nrprot No Hits found

1778.5 Best-BlastP=>>nrprot 52% Identities = 63/115 (54%), Positives = 82/115 (71%), Gaps = 4/115 (3%) ref|NP_215343.1| hypothetical protein Rv0828c [Mycobacterium tuberculosis H37Rv] ref|NP_854509.1| POSSIBLE DEAMINASE [Mycobacterium bovis subsp. bovis AF212297] pir|D70811 hypothetical protein Rv0828c - Mycobacterium tuberculosis (strain H37RV) emb|CAA17634.1| hypothetical protein Rv0828c [Mycobacterium tuberculosis H37Rv] emb|CAD93713.1| POSSIBLE DEAMINASE [Mycobacterium bovis subsp. bovis AF212297] Length = 140

1779.3 Best-BlastP=>>nrprot No Hits found

178.1 Best-BlastP=>>nrprot No Hits found

1780.3 Best-BlastP=>>nrprot 80% Identities = 51/69 (73%), Positives = 56/69 (81%) ref|ZP_00067276.1| COG1278: Cold shock proteins [Microbulbifer degradans 2-40] Length = 71

1781.4 Best-BlastP=>>nrprot 72% Identities = 245/436 (56%), Positives = 318/436 (72%), Gaps = 1/436 (0%) ref|ZP_00031144.1| COG0513: Superfamily II DNA and RNA helicases [Burkholderia fungorum] Length = 534

1782.3 Best-BlastP=>>nrprot 51% Identities = 134/404 (33%), Positives = 216/404 (53%), Gaps = 3/404 (0%) ref|NP_819935.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO90449.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 437

1784.2 Best-BlastP=>>nrprot No Hits found

1786.2 Best-BlastP=>>nrprot 99% Identities = 123/123 (100%), Positives = 123/123 (100%) gb|AAN08839.1| transmission trait enhancer protein LetE [Legionella pneumophila] Length = 123

1787.4 Best-BlastP=>>nrprot 26% Identities = 131/667 (19%), Positives = 275/667 (41%), Gaps = 111/667 (16%) ref|NP_0825559.1| nuclear membrane binding protein NUCLING [Mus musculus] gb|AAH42415.1| Nuclear membrane binding protein NUCLING [Mus musculus] Length = 1413

1788.3 Best-BlastP=>>nrprot 62% Identities = 208/445 (46%), Positives = 285/445 (64%), Gaps = 6/445 (1%) ref|ZP_00118630.1| hypothetical protein [Cytophaga hutchinsonii] Length = 452

179.1 Best-BlastP=>>nrprot 97% Identities = 85/89 (95%), Positives = 88/89 (98%) emb|CAC34415.1| putative TatB protein [Legionella pneumophila] Length = 89

1792.2 Best-BlastP=>>nrprot 46% Identities = 70/254 (27%), Positives = 121/254 (47%), Gaps = 13/254 (5%) ref|NP_421699.1| hypothetical protein [Caulobacter crescentus CB15] pir|[G87608 hypothetical protein CC2905 [imported] - Caulobacter crescentus gb|AAK24867.1| hypothetical protein [Caulobacter crescentus CB15] Length = 261

1793.3 Best-BlastP=>>nrprot 65% Identities = 133/262 (50%), Positives = 182/262 (69%), Gaps = 1/262 (0%) ref|NP_819072.1| xanthosine phosphorylase [Coxiella burnetii RSA 493] gb|AAO89586.1| xanthosine phosphorylase [Coxiella burnetii RSA 493] Length = 273

1794.3 Best-BlastP=>>nrprot 51% Identities = 88/257 (34%), Positives = 132/257 (51%), Gaps = 21/257 (8%) ref|NP_671037.1| 2-deoxyribose-5-phosphate aldolase [Yersinia pestis KIM] gb|AAM87288.1|AE013977_7 2-deoxyribose-5-phosphate aldolase [Yersinia pestis KIM] Length = 270

1795.3 Best-BlastP=>>nrprot 19% Identities = 101/385 (26%), Positives = 172/385 (44%), Gaps = 54/385 (14%) ref|NP_220907.1| unknown [Rickettsia prowazekii] pir|[E71657 hypothetical protein RP534 - Rickettsia prowazekii emb|CAA14983.1| unknown [Rickettsia prowazekii] Length = 598

1797.4 Best-BlastP=>>nrprot 66% Identities = 123/252 (48%), Positives = 174/252 (69%), Gaps = 8/252 (3%) dbj|BAA20497.1| 27kDa outer membrane protein [Coxiella burnetii] Length = 252

18.1 Best-BlastP=>>nrprot No Hits found

180.1 Best-BlastP=>>nrprot 98% Identities = 60/61 (98%), Positives = 61/61 (100%) emb|CAC34414.1| putative TatA protein [Legionella pneumophila] Length = 61

1800.4 Best-BlastP=>>nrprot 74% Identities = 417/723 (57%), Positives = 543/723 (75%), Gaps = 7/723 (0%) ref|NP_407289.1| DNA helicase II [Yersinia pestis] pir|[A|0467 DNA helicase II (EC 3.6.1.-) [imported] - Yersinia pestis (strain CO92) emb|CAC93309.1| DNA helicase II [Yersinia pestis CO92] Length = 720

1803.2 Best-BlastP=>>nrprot 45% Identities = 30/59 (50%), Positives = 40/59 (67%) ref|ZP_00021376.1| COG0477: Permeases of the major facilitator superfamily [Ralstonia metallidurans] Length = 120

1804.2 Best-BlastP=>>nrprot 88% Identities = 320/414 (77%), Positives = 367/414 (88%) gb|AAA92282.1| Hel Length = 414

1805.3 Best-BlastP=>>nrprot 27% Identities = 39/113 (34%), Positives = 59/113 (52%), Gaps = 5/113 (4%) ref|NP_811310.1| conserved hypothetical protein [Bacteroides thetaiotomicron VPI-5482] gb|AAO77504.1| conserved hypothetical protein [Bacteroides thetaiotomicron VPI-5482] Length = 207

1806.2 Best-BlastP=>>nrprot 80% Identities = 90/151 (59%), Positives = 121/151 (80%), Gaps = 3/151 (1%) ref|NP_820500.1| RNA methyltransferase, TrmH family, group 2 [Coxiella burnetii RSA 493] gb|AAO91014.1| RNA methyltransferase, TrmH family, group 2 [Coxiella burnetii RSA 493] Length = 152

1807.3 Best-BlastP=> >nrprot 65% Identities = 221/460 (48%), Positives = 309/460 (67%), Gaps = 2/460 (0%) ref|NP_841539.1| putative homospermidine synthase protein [Nitrosomonas europea ATCC 19718] Length = 472

1809.4 Best-BlastP=> >nrprot 42% Identities = 190/572 (33%), Positives = 326/572 (56%), Gaps = 4/572 (0%) ref|NP_902623.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ60621.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 1390

1812.4 Best-BlastP=> >nrprot 42% Identities = 88/335 (26%), Positives = 168/335 (50%), Gaps = 2/335 (0%) ref|ZP_00092491.1| COG0477: Permeases of the major facilitator superfamily [Azotobacter vinelandii] Length = 432

1815.2 Best-BlastP=> >nrprot 45% Identities = 49/148 (33%), Positives = 80/148 (54%) ref|ZP_00087676.1| COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Pseudomonas fluorescens PfO-1] Length = 167

1817.2 Best-BlastP=> >nrprot No Hits found

1818.4 Best-BlastP=> >nrprot 55% Identities = 280/280 (100%), Positives = 280/280 (100%) emb|CAB65209.1| hypothetical protein [Legionella pneumophila] Length = 280

1819.6 Best-BlastP=> >nrprot 58% Identities = 819/859 (95%), Positives = 836/859 (97%), Gaps = 1/859 (0%) gb|AAD47371.1| LigA [Legionella pneumophila] Length = 869

1823.3 Best-BlastP=> >nrprot 66% Identities = 272/471 (57%), Positives = 367/471 (77%), Gaps = 2/471 (0%) ref|NP_820993.1| ubiquinone biosynthesis protein AarF, putative [Coxiella burnetii] RSA 493] gb|AAO91507.1| ubiquinone biosynthesis protein AarF, putative [Coxiella burnetii RSA 493] Length = 541

1823.5 Best-BlastP=> >nrprot 66% Identities = 206/419 (49%), Positives = 287/419 (68%) ref|NP_252387.1| hypothetical protein [Pseudomonas aeruginosa PA01] pirl|A83183 hypothetical protein PA3697 [Imported] - Pseudomonas aeruginosa (strain PAO1) Length = 431

1826.2 Best-BlastP=> >nrprot No Hits found

1827.3 Best-BlastP=> >nrprot No Hits found

1831.3 Best-BlastP=> >nrprot 73% Identities = 235/399 (58%), Positives = 297/399 (74%) ref|NP_819677.1| riboflavin biosynthesis protein RibA [Coxiella burnetii RSA 493] gb|AAO90191.1| riboflavin biosynthesis protein RibA [Coxiella burnetii RSA 493] Length = 406

1832.4 Best-BlastP=> >nrprot 58% Identities = 82/191 (42%), Positives = 120/191 (62%) ref|NP_819676.1| riboflavin synthase, alpha subunit [Coxiella burnetii RSA 493] gb|AAO90190.1| riboflavin synthase, alpha subunit [Coxiella burnetii RSA 493] Length = 202

1834.4 Best-BlastP=> >nrprot 49% Identities = 144/439 (32%), Positives = 228/439 (51%), Gaps = 14/439 (3%) ref|NP_484368.1| hypothetical protein [Nostoc sp. PCC 7120] pirl|AC1847 hypothetical protein all0324 [Imported] - Nostoc sp. (strain PCC 7120) ORF_ID:all0324~hypothetical protein [Nostoc sp. PCC 7120] Length = 447

1838.2 Best-BlastP=> >nrprot 52% Identities = 170/486 (34%), Positives = 256/486 (52%), Gaps = 27/486 (5%) ref|ZP_00110911.1| COG1816: Adenosine deaminase [Nostoc punctiforme] Length = 523

1839.2 Best-BlastP=> >nrprot 57% Identities = 157/414 (37%), Positives = 230/414 (55%), Gaps = 33/414 (7%) ref|NP_711587.1| sterol desaturase-related protein [Leptospira interrogans serovar Lai str. 56601] gb|AAN48605.1|AE011320_5 sterol desaturase-related protein [Leptospira interrogans serovar Lai str. 56601] Length = 442

184.2 Best-BlastP=> >nrprot No Hits found

1840.3 Best-BlastP=> nrprot 53% Identities = 138/380 (36%), Positives = 220/380 (57%), Gaps = 7/380 (1%) ref|NP_820736.1| drug resistance transporter, Bcr/CfA family [Coxiella burnetii RSA 493] Length = 393

1841.2 Best-BlastP=> nrprot 58% Identities = 215/536 (40%), Positives = 327/536 (61%), Gaps = 9/536 (1%) ref|NP_715995.1| AMP-binding protein [Shewanella oneidensis MR-1] gb|AAN53440.1|AE015483_6 AMP-binding protein [Shewanella oneidensis MR-1] Length = 554

1844.3 Best-BlastP=> nrprot 54% Identities = 120/330 (36%), Positives = 193/330 (58%), Gaps = 3/330 (0%) ref|NP_925659.1| UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Gloeobacter violaceus] dbj|BAC90654.1| UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Gloeobacter violaceus] Length = 345

1845.3 Best-BlastP=> nrprot No Hts found

1846.3 Best-BlastP=> nrprot 62% Identities = 181/411 (44%), Positives = 255/411 (62%), Gaps = 4/411 (0%) gb|AAN87389.1| 3-oxoacyl-[acyl]-carrier-protein synthase [Helicobacillus mobilis] Length = 415

1847.3 Best-BlastP=> nrprot 19% Identities = 77/190 (40%), Positives = 110/190 (57%), Gaps = 5/190 (2%) ref|NP_253486.1| hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9HV11|YBJ8_PSEAE Hypothetical protein PA4798 pir|C83045 hypothetical protein PA4798 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG08184.1|AE004893_2 hypothetical protein PA4798 [Pseudomonas aeruginosa PA01] Length = 242

1848.4 Best-BlastP=> nrprot 31% Identities = 77/258 (29%), Positives = 129/258 (50%), Gaps = 21/258 (8%) ref|NP_832609.1| Methyltransferase [Bacillus cereus ATCC 14579] gb|AAP09810.1| Methyltransferase [Bacillus cereus ATCC 14579] Length = 253

1849.3 Best-BlastP=> nrprot 40% Identities = 45/134 (33%), Positives = 73/134 (54%), Gaps = 4/134 (2%) ref|NP_636084.1| acetyltransferase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM40008.1| acetyltransferase [Xanthomonas campestris pv. campestris] Length = 157

1851.1 Best-BlastP=> nrprot 69% Identities = 141/253 (55%), Positives = 182/253 (71%), Gaps = 1/253 (0%) ref|NP_484519.1| probable short-chain dehydrogenase [Nostoc sp. PCC 7120] pir|AB1866 hypothetical protein all0475 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB72433.1| ORF_ID:all0475~probable short-chain dehydrogenase [Nostoc sp. PCC 7120] Length = 257

1852.2 Best-BlastP=> nrprot 54% Identities = 43/110 (39%), Positives = 65/110 (59%), Gaps = 6/110 (5%) ref|NP_900345.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58351.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 128

1853.2 Best-BlastP=> nrprot 58% Identities = 65/127 (51%), Positives = 79/127 (62%), Gaps = 9/127 (7%) ref|NP_459344.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] gb|AAL19303.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] Length = 119

1856.3 Best-BlastP=> nrprot No Hts found

1858.1 Best-BlastP=> nrprot 51% Identities = 85/271 (31%), Positives = 139/271 (51%), Gaps = 21/271 (7%) ref|NP_219985.1| hypothetical protein [Chlamydia trachomatis] pir|E71509 hypothetical protein CT472 - Chlamydia trachomatis (serotype D, hypothetical protein [Chlamydia trachomatis] Length = 264

1860.2 Best-BlastP=> >nprot 47% Identities = 104/344 (30%), Positives = 174/344 (50%), Gaps = 38/344 (11%) gb|AAF86695.1|AF180956_1 AMPC cephalosporinase precursor protein ACC-3a [Hafnia alvei] Length = 377

1861.2 Best-BlastP=> >nprot No Hits found

1862.2 Best-BlastP=> >nprot 63% Identities = 206/470 (43%), Positives = 279/470 (59%), Gaps = 41/470 (8%) ref|NP_249771.1| flagellar hook protein FlgE [Pseudomonas aeruginosa PA01] pir|F83510 flagellar hook protein FlgE PA1080 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04469.1|AE004539_11 flagellar hook protein FlgE [Pseudomonas aeruginosa PAO1] Length = 462

1863.2 Best-BlastP=> >nprot 64% Identities = 97/223 (43%), Positives = 145/223 (65%), Gaps = 2/223 (0%) ref|ZP_00138665.1| COG1843: Flagellar hook capping protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 237

1864.3 Best-BlastP=> >nprot 73% Identities = 273/454 (60%), Positives = 346/454 (76%), Gaps = 5/454 (1%) ref|NP_638130.1| succinyl-diaminopimelate desuccinylase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42054.1| succinyl-diaminopimelate campestris str. ATCC 33913] Length = 497

1865.3 Best-BlastP=> >nprot 72% Identities = 175/353 (49%), Positives = 263/353 (74%), Gaps = 1/353 (0%) ref|NP_562979.1| UDP-N-acetylglucosamine-N-acetylglucosaminyl-(pentapeptide) pyrophosphoryl N-acetylglucosamine transferase [Clostridium perfringens] sp|Q8X1Q1|MURG_CLOPE UDP-N-acetylglucosamine--N-acetylglucosaminyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Undecaprenyl-PP-MurNAc-pentapeptide-UDP-GlcNAc GlcNAc transferase) dbj|BAB81769.1| UDP-N-acetylglucosamine-N-acetylglucosaminyl-(pentapeptide) pyrophosphoryl N-acetylglucosamine transferase [Clostridium perfringens str. 13] Length = 357

1871.1 Best-BlastP=> >nprot No Hits found

1870.3 Best-BlastP=> >nprot 60% Identities = 152/349 (43%), Positives = 223/349 (63%), Gaps = 19/349 (5%) ref|NP_767636.1| HlyD family secretion protein [Bradyrhizobium japonicum] dbj|BAC46261.1| HlyD family secretion protein [Bradyrhizobium japonicum USDA 110] Length = 410

1871.2 Best-BlastP=> >nprot 99% Identities = 348/348 (100%), Positives = 348/348 (100%) emb|CAC33484.1| RecA protein [Legionella pneumophila] Length = 348

1873.2 Best-BlastP=> >nprot 99% Identities = 150/150 (100%), Positives = 150/150 (100%) sp|P37864|RECX_LEGPN Regulatory protein recX emb|CAC33485.1| RecX protein [Legionella pneumophila] Length = 150

1875.2 Best-BlastP=> >nprot 75% Identities = 234/379 (61%), Positives = 294/379 (77%) ref|NP_842481.1| General substrate transporters [Nitrosomonas europaea ATCC 19718] emb|CAD86404.1| General substrate transporters [Nitrosomonas europaea ATCC 19718] Length = 391

1878.3 Best-BlastP=> >nprot 63% Identities = 130/311 (41%), Positives = 199/311 (63%), Gaps = 7/311 (2%) ref|NP_520407.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD15993.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 317

188.1 Best-BlastP=> >nprot No Hits found

1880.3 Best-BlastP=> >nprot 79% Identities = 208/324 (64%), Positives = 262/324 (80%) ref|NP_820236.1| malate dehydrogenase [Coxiella burnetii RSA 493] gb|AAO90750.1| malate dehydrogenase [Coxiella burnetii RSA 493] Length = 328

1882.2 Best-BlastP=> >nrprot 52% Identities = 116/255 (45%), Positives = 165/255 (64%), Gaps = 12/255 (4%) ref|NP_819457.1| polysaccharide deacetylase-related protein [Coxiella burnetii RSA 493] Length = 276

1883.4 Best-BlastP=> >nrprot No Hits found

1885.3 Best-BlastP=> >nrprot 67% Identities = 221/446 (49%), Positives = 307/446 (68%), Gaps = 5/446 (1%) ref|NP_252709.1| UDP-N-acetylglucosamine:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [Pseudomonas aeruginosa PA01] pir|A83145 UDP-N-acetylglucosamine:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) PA4020 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG07407.1|AE004818_13 UDP-N-acetylglucosamine:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [Pseudomonas aeruginosa PA01] Length = 451

1886.2 Best-BlastP=> >nrprot No Hits found

1887.2 Best-BlastP=> >nrprot 37% Identities = 126/504 (25%), Positives = 205/504 (40%), Gaps = 128/504 (25%) ref|NP_905954.1| leucine-rich protein [Porphyromonas gingivalis W83] gb|AAQ66853.1| leucine-rich protein [Porphyromonas gingivalis W83] Length = 1266

1889.2 Best-BlastP=> >nrprot 30% Identities = 64/297 (21%), Positives = 122/297 (41%), Gaps = 33/297 (11%) ref|NP_764683.1| ebbA protein [Staphylococcus epidermidis ATCC 12228] gb|AAO04725.1|AE016747_222 ebbA protein [Staphylococcus epidermidis ATCC 12228] Length = 9439

189.3 Best-BlastP=> >nrprot 81% Identities = 272/394 (69%), Positives = 330/394 (83%) dbl|BAB55449.1| NAD+-dependent formate dehydrogenase [Hypomicrobium sp. JC17] Length = 399

1891.2 Best-BlastP=> >nrprot 47% Identities = 72/239 (30%), Positives = 123/239 (51%) ref|NP_812276.1| hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO078470.1| hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Length = 247

1893.2 Best-BlastP=> >nrprot 64% Identities = 98/218 (44%), Positives = 142/218 (65%), Gaps = 2/218 (0%) ref|NP_820819.1| ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5 [Coxiella burnetii RSA 493] gb|AAO91333.1| ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5 [Coxiella burnetii RSA 493] Length = 244

1894.2 Best-BlastP=> >nrprot 73% Identities = 63/101 (62%), Positives = 76/101 (75%) ref|ZP_000086202.1| COG0261: Ribosomal protein L21 [Pseudomonas fluorescens PfO-1] Length = 103

1895.6 Best-BlastP=> >nrprot 47% Identities = 59/173 (34%), Positives = 100/173 (57%), Gaps = 14/173 (8%) ref|NP_842310.1| putative type 4 fimbrial biogenesis protein PilP [Nitrosomonas europaea ATCC 19718] emb|CAD86225.1| putative type 4 fimbrial biogenesis protein PilP [Nitrosomonas europaea ATCC 19718] Length = 176

1896.5 Best-BlastP=> >nrprot 61% Identities = 282/695 (40%), Positives = 430/695 (61%), Gaps = 40/695 (5%) ref|NP_715925.1| type IV pilus biogenesis protein PilQ [Shewanella oneidensis MR-1] gb|AN53370.1|AE015476_11 type IV pilus biogenesis protein PilQ [Shewanella oneidensis MR-1] Length = 684

19.1 Best-BlastP=> >nrprot 37% Identities = 48/174 (27%), Positives = 80/174 (45%), Gaps = 14/174 (8%) ref|NP_820400.1| peptidase, family S24 [Coxiella burnetii RSA 493] gb|AAO90914.1| peptidase, family S24 [Coxiella burnetii RSA 493] Length = 216

190.3 Best-BlastP=> >nrprot No Hits found

1902.5 Best-BlastP=> >nrprot 79% Identities = 205/338 (60%), Positives = 264/338 (78%), Gaps = 5/338 (1%) ref|ZP_00086819.1| COG0533: Metal-dependent proteases with possible chaperone activity [Pseudomonas fluorescens PfO-1] Length = 341

1903.4 Best-BlastP=>>nrprot 58% Identities = 119/287 (41%), Positives = 161/287 (56%), Gaps = 14/287 (4%) ref|NP_821016.1| chitinase domain protein [Coxiella burnetii RSA 493] gb|AAO91530.1| chitinase domain protein [Coxiella burnetii RSA 493] Length = 593

1905.2 Best-BlastP=>>nrprot 77% Identities = 248/422 (58%), Positives = 328/422 (77%), Gaps = 1/422 (0%) ref|NP_718455.1| conserved hypothetical protein [Shewanella oneidensis MR-1] sp|P59352|YS83_SHEON Hypothetical UPF0229 protein SO2883 gb|AAN55899.1|AE015726_7 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 422

1906.2 Best-BlastP=>>nrprot 83% Identities = 347/504 (68%), Positives = 425/504 (84%), Gaps = 1/504 (0%) ref|NP_790392.1| SpoVR like family protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54087.1| SpoVR like family protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 520

1908.4 Best-BlastP=>>nrprot 60% Identities = 348/811 (42%), Positives = 495/811 (61%), Gaps = 14/811 (1%) emb|CAD58321.1| Long chain acyl-CoA dehydrogenase [Azoarcus sp. EbN1] Length = 829

191.1 Best-BlastP=>>nrprot 50% Identities = 76/297 (25%), Positives = 144/297 (48%), Gaps = 33/297 (11%) ref|NP_832129.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] gb|AAP09330.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] Length = 300

1910.6 Best-BlastP=>>nrprot 12% Identities = 92/441 (20%), Positives = 185/441 (41%), Gaps = 64/441 (14%) gb|AAB70839.1| ZipA [Dictyostelium discoideum] Length = 924

1911.4 Best-BlastP=>>nrprot 41% Identities = 37/110 (33%), Positives = 64/110 (58%), Gaps = 6/110 (5%) ref|ZP_00054083.1| cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Magnospirillum magnetotacticum] Length = 282

1913.2 Best-BlastP=>>nrprot 61% Identities = 41/91 (45%), Positives = 61/91 (67%) ref|NP_819252.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89766.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 130

1915.3 Best-BlastP=>>nrprot 56% Identities = 237/625 (37%), Positives = 364/625 (58%), Gaps = 18/625 (2%) ref|NP_518200.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD13607.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 795

1918.3 Best-BlastP=>>nrprot 74% Identities = 142/226 (62%), Positives = 176/226 (77%), Gaps = 1/226 (0%) ref|NP_384333.1| PUTATIVE TRANSCRIPTION REGULATOR PROTEIN [Sinorhizobium meliloti] Length = 230

1920.3 Best-BlastP=>>nrprot 66% Identities = 198/345 (57%), Positives = 239/345 (69%), Gaps = 9/345 (2%) emb|CAB82454.1| CnrT protein [Ralstonia metallidurans] Length = 351

1923.2 Best-BlastP=>>nrprot No Hits found

1924.4 Best-BlastP=>>nrprot 62% Identities = 75/165 (45%), Positives = 106/165 (64%), Gaps = 6/165 (3%) ref|NP_840350.1| putative antirestriction protein [Nitrosomonas europaea ATCC 19718] emb|CAD84171.1| putative antirestriction protein [Nitrosomonas europaea ATCC 19718] Length = 171

1926.2 Best-BlastP=>>nrprot 71% Identities = 121/188 (64%), Positives = 150/188 (79%), Gaps = 1/188 (0%) ref|NP_405720.1| thymidine kinase [Yersinia pestis] ref|NP_669456.1| thymidine kinase [Yersinia pestis KIM] sp|Q8ZEJ1|KITH_YERPE Thymidine kinase pir|AD0265 thymidine kinase (EC 2.7.1.21) [similarity] - Yersinia pestis (strain CO92) emb|CAC90984.1| thymidine kinase [Yersinia pestis CO92] gb|AAM85707.1|AE013818_1 thymidine kinase [Yersinia pestis KIM] Length = 196

1928.2 Best-BlastP=> >nrprot 60% Identities = 181/408 (44%), Positives = 254/408 (62%), Gaps = 8/408 (1%) ref|NP_821038.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAC091552.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 446

193.3 Best-BlastP=> >nrprot 56% Identities = 132/320 (41%), Positives = 199/320 (62%), Gaps = 17/320 (5%) gb|AAC21671.1| PvcA [Pseudomonas aeruginosa]

1930.3 Best-BlastP=> >nrprot No Hits found

1933.4 Best-BlastP=> >nrprot 14% Identities = 109/524 (20%), Positives = 228/524 (43%), Gaps = 74/524 (14%) ref|NP_010225.1| involved in intracellular protein transport, coiled-coil protein necessary for protein transport from ER to Golgi; Uso1p [Saccharomyces cerevisiae] pirl|S67593 transport protein USO1 - yeast (Saccharomyces cerevisiae) emb|CAA98621.1| USO1 [Saccharomyces cerevisiae] Length = 1790

1934.4 Best-BlastP=> >nrprot 97% Identities = 310/333 (93%), Positives = 324/333 (97%) emb|CAB65198.1| hypothetical protein [Legionella pneumophila] Length = 333

1935.4 Best-BlastP=> >nrprot 96% Identities = 348/372 (93%), Positives = 360/372 (96%), Gaps = 3/372 (0%) emb|CAB65199.1| hypothetical protein [Legionella pneumophila] Length = 369

1937.4 Best-BlastP=> >nrprot No Hits found

1939.5 Best-BlastP=> >nrprot No Hits found

1940.2 Best-BlastP=> >nrprot 53% Identities = 153/524 (29%), Positives = 286/524 (54%), Gaps = 30/524 (5%) ref|NP_922967.1| HlyB/MsbA family ABC transporter [Gloeoibacter violaceus] dbj|BAC87962.1| HlyB/MsbA family ABC transporter [Gloeoibacter violaceus] Length = 605

1943.3 Best-BlastP=> >nrprot 55% Identities = 136/303 (44%), Positives = 183/303 (60%), Gaps = 3/303 (0%) ref|ZP_00095364.1| COG0845: Membrane-fusion protein [Novosphingobium aromaticivorans] Length = 371

1945.4 Best-BlastP=> >nrprot 80% Identities = 408/591 (69%), Positives = 473/591 (80%), Gaps = 5/591 (0%) ref|NP_706511.1| succinate dehydrogenase flavoprotein subunit [Shigella flexneri 2a str. 301] gb|AN42218.1|AE015088_5 succinate dehydrogenase flavoprotein subunit [Shigella flexneri 2a str. 301] Length = 592

1946.2 Best-BlastP=> >nrprot 78% Identities = 156/227 (68%), Positives = 188/227 (82%), Gaps = 1/227 (0%) emb|CAA74088.1| succinate dehydrogenase putative iron sulphur subunit [Shewanella frigidimarina] Length = 235

1947.3 Best-BlastP=> >nrprot 45% Identities = 76/274 (27%), Positives = 133/274 (48%), Gaps = 12/274 (4%) ref|ZP_00069289.1| COG1577: Mevalonate kinase [Oenococcus oeni MCW] Length = 306

1949.4 Best-BlastP=> >nrprot 67% Identities = 38/83 (45%), Positives = 61/83 (73%) ref|NP_252324.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] pirl|G83191 conserved hypothetical protein PA3634 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AG07022.1|AE004783_7 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 94

195.3 Best-BlastP=> >nrprot 79% Identities = 181/278 (65%), Positives = 223/278 (80%) ref|NP_231578.1| PvcB protein [Vibrio cholerae O1 biovar eltor str. N16961] pirl|B82137 PvcB protein VC1944 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95092.1| PvcB protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 287

1950.2 Best-BlastP=>>nrprot 55% Identities = 159/405 (39%), Positives = 239/405 (59%), Gaps = 13/405 (3%) refINP_820347.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90861.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 426

1951.4 Best-BlastP=>>nrprot 81% Identities = 170/245 (69%), Positives = 205/245 (83%) refINP_924317.1| probable ABC transporter ATP-binding protein [Gloeobacter violaceus] dbj|BAC89312.1| gtr1371 [Gloeobacter violaceus] Length = 252

1955.3 Best-BlastP=>>nrprot 46% Identities = 141/475 (29%), Positives = 221/475 (46%), Gaps = 64/475 (13%) refZP_00015335.1| COG2067: Long-chain fatty acid transport protein [Rhodospirillum rubrum] Length = 436

1960.2 Best-BlastP=>>nrprot No Hits found

1961.3 Best-BlastP=>>nrprot 96% Identities = 283/293 (96%), Positives = 284/293 (96%) gb|AAM00623.1| unknown [Legionella pneumophila] Length = 293

1966.2 Best-BlastP=>>nrprot 84% Identities = 131/188 (69%), Positives = 160/188 (85%) refINP_820795.1| translation elongation factor P [Coxiella burnetii RSA 493] gb|AAO91309.1| translation elongation factor P [Coxiella burnetii RSA 493] Length = 188

1968.1 Best-BlastP=>>nrprot 41% Identities = 25/64 (39%), Positives = 32/64 (50%), Gaps = 13/64 (20%) refZP_00011706.1| hypothetical protein [Rhodopseudomonas palustris] Length = 150

197.3 Best-BlastP=>>nrprot 80% Identities = 324/474 (68%), Positives = 389/474 (82%) refINP_231579.1| FAD monooxygenase, PheA/TfdB family [Vibrio cholerae O1 biovar eltor str. N16961] pirl|C82137 FAD monooxygenase, PheA/TfdB family VC1945 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95093.1| FAD monooxygenase, PheA/TfdB family [Vibrio cholerae O1 biovar eltor str. N16961] Length = 487

1972.3 Best-BlastP=>>nrprot 62% Identities = 158/342 (46%), Positives = 216/342 (63%), Gaps = 3/342 (0%) gb|AAP58486.1| putative phosphoribosylformylglycinamide cyclo ligase [uncultured Acidobacteria bacterium] Length = 343

1976.2 Best-BlastP=>>nrprot 79% Identities = 427/626 (68%), Positives = 497/626 (79%), Gaps = 6/626 (0%) refINP_720274.1| glucose-inhibited division protein A [Shewanella oneidensis MR-1] gb|AN57717.1|AE015908_2 glucose-inhibited division protein A [Shewanella oneidensis MR-1] Length = 629

1978.1 Best-BlastP=>>nrprot 63% Identities = 94/201 (46%), Positives = 133/201 (66%), Gaps = 6/201 (2%) refINP_246425.1| GidB [Pasteurella multocida] sp|P57946|GIDB_PASMU Methyltransferase gidB (Glucose inhibited division protein B) gb|AAK03570.1| GidB [Pasteurella multocida] Length = 210

1979.1 Best-BlastP=>>nrprot 79% Identities = 163/254 (64%), Positives = 204/254 (80%) refINP_820903.1| sporulation initiation inhibitor protein soj [Coxiella burnetii RSA 493] gb|AAO91417.1| sporulation initiation inhibitor protein soj [Coxiella burnetii RSA 493] Length = 256

1983.1 Best-BlastP=>>nrprot 63% Identities = 138/265 (52%), Positives = 175/265 (66%), Gaps = 1/265 (0%) refINP_820962.1| bis(5'-nucleosyl)-tetraphosphatase, symmetrical [Coxiella burnetii RSA 493] sp|Q83AB7|APAH_COXBU Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5"-P1,P4-tetraphosphate pyrophosphohydrolase) gb|AAO91476.1| bis(5'-nucleosyl)-tetraphosphatase, symmetrical [Coxiella burnetii RSA 493] Length = 291

1986.2 Best-BlastP=>>nrprot 24% Identities = 56/235 (23%), Positives = 111/235 (47%), Gaps = 11/235 (4%) gb|AAP84130.1| putative pathogenesis-related protein [Pseudomonas aeruginosa] Length = 639

1989.2 Best-BlastP=>>nrprot 70% Identities = 263/481 (54%), Positives = 348/481 (72%), Gaps = 1/481 (0%) sp|P37986|G6PD_ERWCH Glucose-6-phosphate 1-dehydrogenase (G6PD) pir||S337053 glucose-6-phosphate 1-dehydrogenase [Erwinia chrysanthemi] emb|CAA52858.1| glucose-6-phosphate 1-dehydrogenase [Erwinia chrysanthemi] Length = 491

199.1 Best-BlastP=>>nrprot 45% Identities = 105/371 (28%), Positives = 173/371 (46%), Gaps = 13/371 (3%) ref|ZP_00014611.1| COG2814: Arabinose efflux permease [Rhodospirillum rubrum] Length = 411

1990.1 Best-BlastP=>>nrprot 55% Identities = 102/228 (44%), Positives = 136/228 (59%), Gaps = 2/228 (0%) gb|AAL76390.1| 6-phosphogluconactonase [uncultured proteobacterium] Length = 226

1992.2 Best-BlastP=>>nrprot No Hits found

1998.3 Best-BlastP=>>nrprot 51% Identities = 119/265 (44%), Positives = 170/265 (64%), Gaps = 9/265 (3%) ref|ZP_00089281.1| COG1295: Predicted membrane protein [Azotobacter vinelandii] Length = 408

2.1 Best-BlastP=>>nrprot 59% Identities = 70/170 (41%), Positives = 102/170 (60%), Gaps = 2/170 (1%) ref|NP_907750.1| HYPOTHETICAL PROTEIN-RecB family exonuclease [succinogenes] emb|CAE10650.1| HYPOTHETICAL PROTEIN-RecB family exonuclease [Wolinella succinogenes] Length = 193

20.1 Best-BlastP=>>nrprot No Hits found

2000.1 Best-BlastP=>>nrprot 99% Identities = 149/149 (100%), Positives = 149/149 (100%) gb|AAC38305.1| type IV pilin; competence and adherence associated pilin; CAP [Legionella pneumophila] Length = 149

2006.2 Best-BlastP=>>nrprot 46% Identities = 64/229 (27%), Positives = 102/229 (44%), Gaps = 27/229 (11%) ref|NP_762597.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO07587.1|AE016810_90 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 232

2007.1 Best-BlastP=>>nrprot 72% Identities = 173/298 (58%), Positives = 220/298 (73%) ref|NP_792548.1| hydroxymethylglutaryl-CoA lyase [Pseudomonas syringae pv. tomato str. DC3000] Length = 299

201.2 Best-BlastP=>>nrprot 50% Identities = 139/407 (34%), Positives = 209/407 (51%), Gaps = 9/407 (2%) dbj|BAB69410.1| hypothetical protein [Streptomyces avermitilis] Length = 468

2016.2 Best-BlastP=>>nrprot 64% Identities = 54/141 (38%), Positives = 90/141 (63%), Gaps = 4/141 (2%) ref|NP_820504.1| rhodanese domain protein [Coxiella burnetii RSA 493] gb|AAQ91018.1| rhodanese domain protein [Coxiella burnetii RSA 493] Length = 144

2017.1 Best-BlastP=>>nrprot 52% Identities = 70/179 (39%), Positives = 99/179 (55%), Gaps = 7/179 (3%) ref|ZP_00124407.1| COG2840: Uncharacterized protein conserved in bacteria [Pseudomonas syringae pv. syringae B728a] Length = 185

2019.2 Best-BlastP=>>nrprot 61% Identities = 112/266 (42%), Positives = 153/266 (57%), Gaps = 28/266 (10%) ref|NP_253119.1| probable cytochrome c1 precursor [Pseudomonas aeruginosa PA01] pir||E83092 probable cytochrome c1 precursor PA4429 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07817.1|AE004857_8 probable cytochrome c1 precursor [Pseudomonas aeruginosa PAO1] Length = 260

202.3 Best-BlastP=>>nrprot 57% Identities = 299/765 (39%), Positives = 444/765 (58%), Gaps = 17/765 (2%) ref|NP_519533.1| PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] emb|CAD15114.1| PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] Length = 765

2020.1 Best-BlastP=> >nrprot 78% Identities = 128/206 (62%), Positives = 163/206 (79%), Gaps = 2/206 (0%) ref|NP_716244.1| stringent starvation protein a [Shewanella oneidensis MR-1] gb|AN53689.1|AE015508_5 stringent starvation protein a [Shewanella oneidensis MR-1] Length = 209

2021.1 Best-BlastP=> >nrprot 67% Identities = 68/134 (50%), Positives = 89/134 (66%), Gaps = 5/134 (3%) ref|NP_820726.1| stringent starvation protein B [Coxiella burnetii RSA 493] gb|AAO91240.1| stringent starvation protein B [Coxiella burnetii RSA 493] Length = 138

2022.1 Best-BlastP=> >nrprot No Hits found

2024.2 Best-BlastP=> >nrprot 58% Identities = 66/177 (37%), Positives = 105/177 (59%) ref|ZP_00065967.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 183

2026.1 Best-BlastP=> >nrprot No Hits found

2027.2 Best-BlastP=> >nrprot 50% Identities = 140/413 (33%), Positives = 215/413 (52%), Gaps = 13/413 (3%) ref|NP_215111.1| hypothetical protein Rv0597c [Mycobacterium tuberculosis H37Rv] ref|NP_335037.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] ref|NP_854272.1| CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] pir|H70908 hypothetical protein Rv0597c - Mycobacterium tuberculosis (strain H37Rv) emb|CAB09957.1| hypothetical protein Rv0597c [Mycobacterium tuberculosis H37Rv] gb|AAK44851.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] emb|CAD93475.1| CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] Length = 411

2029.2 Best-BlastP=> >nrprot No Hits found

2030.2 Best-BlastP=> >nrprot No Hits found

2031.2 Best-BlastP=> >nrprot 31% Identities = 24/63 (38%), Positives = 36/63 (57%) ref|NP_051664.1| transposase, putative [Deinococcus radiodurans] pir|A75633 probable transposase - Deinococcus radiodurans (strain R1) gb|AAF12606.1|AE001826_75 transposase, putative [Deinococcus radiodurans] Length = 327

2034.2 Best-BlastP=> >nrprot 40% Identities = 65/223 (29%), Positives = 110/223 (49%), Gaps = 13/223 (5%) ref|ZP_00009418.1| COG1647: Esterase/lipase [Rhodopseudomonas palustris] Length = 263

2037.3 Best-BlastP=> >nrprot 97% Identities = 453/469 (96%), Positives = 459/469 (97%) gb|AAM00645.1| Zn metalloprotein [Legionella pneumophila] Length = 469

2039.1 Best-BlastP=> >nrprot No Hits found

204.1 Best-BlastP=> >nrprot 63% Identities = 199/448 (44%), Positives = 288/448 (64%), Gaps = 1/448 (0%) ref|NP_459228.1| putative membrane-associated Zn-dependent protease [Salmonella typhimurium LT2] sp|Q8ZRP1|ECFE_SALTY Protease ecfE gb|AAL19187.1| putative membrane-associated Zn-dependent protease [Salmonella typhimurium LT2] Length = 450

2041.2 Best-BlastP=> >nrprot 36% Identities = 74/238 (31%), Positives = 119/238 (50%), Gaps = 4/238 (1%) gb|AAK19894.1| O-methyltransferase [Polyangium cellulosum] Length = 346

2044.2 Best-BlastP=> >nrprot 59% Identities = 274/627 (43%), Positives = 384/627 (61%), Gaps = 9/627 (1%) sp|Q59118|AMOH_ARTGO Histamine oxidase (Copper amine oxidase) pir|A56102 amine oxidase (copper-containing) (EC 1.4.3.6) - Arthrobacter globiformis dbj|BA07517.1| Copper amine oxidase, Monoamine oxidase, Histamine oxidase [Arthrobacter globiformis] Length = 684

2049.2 Best-BlastP=>>nrprot 26% Identities = 57/288 (19%), Positives = 112/288 (38%), Gaps = 32/288 (11%) pirl|T13030 microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster) gb|AAB96783.1| microtubule binding protein D-CLIP-190 [Drosophila melanogaster]
Length = 1690

2051.1 Best-BlastP=>>nrprot 59% Identities = 103/267 (38%), Positives = 158/267 (59%), Gaps = 15/267 (5%) ref|NP_820370.1| phosphatidate cytidylyltransferase [Coxiella burnetii RSA 493] gb|AAO90884.1| phosphatidate cytidylyltransferase [Coxiella burnetii RSA 493] Length = 272

2051.2 Best-BlastP=>>nrprot 37% Identities = 34/108 (31%), Positives = 63/108 (58%), Gaps = 2/108 (1%) ref|NP_932218.1| putative conjugative transfer protein TrbB [Vibrio vulnificus YJ016] dbj|BAC97741.1| putative conjugative transfer protein TrbB [Vibrio vulnificus YJ016] Length = 137

2053.2 Best-BlastP=>>nrprot 55% Identities = 146/331 (44%), Positives = 180/331 (54%), Gaps = 57/331 (17%) gb|AAC83331.1| major outer membrane protein precursor [Legionella pneumophila] Length = 288

2054.2 Best-BlastP=>>nrprot 54% Identities = 128/296 (43%), Positives = 184/296 (62%), Gaps = 17/296 (5%) ref|NP_442548.1| unknown protein [Synechocystis sp. PCC 6803] pirl|S76674 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10618.1| srl0619 [Synechocystis sp. PCC 6803] Length = 348

2056.1 Best-BlastP=>>nrprot 55% Identities = 109/292 (37%), Positives = 165/292 (56%), Gaps = 8/292 (2%) ref|ZP_00134420.1| COG0500: SAM-dependent methyltransferases [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 290

2057.3 Best-BlastP=>>nrprot 59% Identities = 145/350 (41%), Positives = 208/350 (59%), Gaps = 17/350 (4%) ref|ZP_00097544.1| COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Desulfitobacterium hafniense] Length = 342

206.3 Best-BlastP=>>nrprot 66% Identities = 120/227 (52%), Positives = 150/227 (66%) ref|NP_252342.1| undecaprenyl pyrophosphate synthetase [Pseudomonas aeruginosa PA01] pirl|G83188 undecaprenyl pyrophosphate synthetase PA3652 [Imported] - (strain PAO1) gb|AAG07040.1|AE004785_4 undecaprenyl pyrophosphate synthetase [Pseudomonas aeruginosa PA01] Length = 251

2060.3 Best-BlastP=>>nrprot 32% Identities = 71/221 (32%), Positives = 123/221 (55%), Gaps = 24/221 (10%) ref|ZP_00082359.1| COG2199: FOG: GGDEF domain [Geobacter metallireducens] Length = 353

2062.2 Best-BlastP=>>nrprot No Hits found

2064.3 Best-BlastP=>>nrprot No Hits found

2065.2 Best-BlastP=>>nrprot No Hits found

2066.5 Best-BlastP=>>nrprot No Hits found

2067.5 Best-BlastP=>>nrprot 61% Identities = 151/349 (43%), Positives = 215/349 (61%), Gaps = 19/349 (5%) ref|NP_660996.1| glycosyl hydrolase, family 3 [Chlorobium tepidum TLS] gb|AAM71338.1| glycosyl hydrolase, family 3 [Chlorobium tepidum TLS] Length = 372

2068.3 Best-BlastP=>>nrprot 27% Identities = 71/336 (21%), Positives = 133/336 (39%), Gaps = 67/336 (19%) emb|CAE02882.1| OSJNBB0022F23.19 [Oryza sativa (japonica cultivar-group)] Length = 2391

207.3 Best-BlastP=>>nrprot 98% Identities = 418/423 (98%), Positives = 419/423 (99%) gb|AAM73854.1|AF454865_1 putative phospholipase C [Legionella pneumophila] Length = 423

2070.4 Best-BlastP=> >nrprot 49% Identities = 166/568 (29%), Positives = 274/568 (48%), Gaps = 46/568 (8%) refINP_251765.1| hypothetical protein [Pseudomonas aeruginosa PA01] ref|ZP_00136432.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] pir|D83262 hypothetical protein PA3075 [imported] - Pseudomonas aeruginosa PA01] Length = 543

2073.4 Best-BlastP=> >nrprot 37% Identities = 49/192 (25%), Positives = 85/192 (44%), Gaps = 23/192 (11%) refINP_929249.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TT01] emb|CAE14276.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TT01] Length = 231

2075.1 Best-BlastP=> >nrprot No Hits found

2078.2 Best-BlastP=> >nrprot No Hits found

2079.2 Best-BlastP=> >nrprot No Hits found

2080.3 Best-BlastP=> >nrprot 57% Identities = 88/221 (39%), Positives = 128/221 (57%), Gaps = 1/221 (0%) refINP_925444.1| hypothetical protein gll|2498 [Gloeo bacter violaceus] dbj|BAC90439.1| gll|2498 [Gloeo bacter violaceus] Length = 222

2082.2 Best-BlastP=> >nrprot 75% Identities = 34/66 (51%), Positives = 51/66 (77%) refINP_768003.1| bsl|1363 [Bradyrhizobium japonicum] dbj|BAC46628.1| bsl|1363 [Bradyrhizobium japonicum USDA 110] Length = 73

2083.2 Best-BlastP=> >nrprot 98% Identities = 224/227 (98%), Positives = 226/227 (99%) gbl|AAM00399.1|AF386079_9 CcmH [Legionella pneumophila] Length = 360

2085.2 Best-BlastP=> >nrprot 99% Identities = 132/133 (99%), Positives = 133/133 (100%) gbl|AAM00399.1|AF386079_9 CcmH [Legionella pneumophila] Length = 360

2087.2 Best-BlastP=> >nrprot 36% Identities = 88/166 (53%), Positives = 116/166 (69%) refINP_819420.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gbl|AAO89934.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 176

209.2 Best-BlastP=> >nrprot 24% Identities = 41/135 (30%), Positives = 61/135 (45%), Gaps = 36/135 (26%) gbl|AAO49307.1| outer surface protein precursor [Wolbachia pipiensis] Length = 186

2091.1 Best-BlastP=> >nrprot 39% Identities = 60/226 (26%), Positives = 99/226 (43%), Gaps = 8/226 (3%) gbl|AAK31375.1|AC084329_1 ppg3 [Leishmania major] Length = 1325

2092.2 Best-BlastP=> >nrprot 86% Identities = 634/850 (74%), Positives = 741/850 (87%) refINP_457131.1| ClpB protein (heat shock protein f84.1) [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_461591.1| ATP-dependent protease, Hsp 100, part of novel multi-chaperone system with DnaK, DnaJ, and GrpE [Salmonella typhimurium LT2] ref|NP_806327.1| ClpB protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|AI0831 ClpB protein (heat shock protein f84.1) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain C718) gbl|AAL21550.1| ATP-dependent protease [Salmonella typhimurium LT2] emb|CAD05840.1| ClpB protein (heat shock protein f84.1) [Salmonella enterica subsp. enterica serovar Typhi] Length = 857

2095.2 Best-BlastP=> >nrprot 72% Identities = 218/393 (55%), Positives = 285/393 (72%), Gaps = 1/393 (0%) ref|ZP_00125180.1| COG2081: Predicted flavoproteins [Pseudomonas syringae pv. syringae B728a] Length = 392

2098.2 Best-BlastP=> >nrprot No Hits found

2103.2 Best-BlastP=>>nprot 69% Identities = 424/791 (53%), Positives = 552/791 (69%), Gaps = 3/791 (0%) refINP_637344.1| 3-hydroxyacyl-CoA dehydrogenase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM41268.1| 3-hydroxyacyl-CoA dehydrogenase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 790

2104.1 Best-BlastP=>>nprot 85% Identities = 91/127 (71%), Positives = 108/127 (85%), Gaps = 1/127 (0%) refINP_878931.1| 50S ribosomal protein L7/L12 [Bordetella pertussis] refINP_882379.1| 50S ribosomal protein L7/L12 [Bordetella parapertussis] refINP_886566.1| 50S ribosomal protein L7/L12 [Bordetella bronchiseptica] emb|CAE39754.1| 50S ribosomal protein L7/L12 [Bordetella parapertussis] emb|CAE40393.1| 50S ribosomal protein L7/L12 [Bordetella pertussis] emb|CAE30515.1| 50S ribosomal protein L7/L12 [Bordetella bronchiseptica] Length = 127

2106.2 Best-BlastP=>>nprot 73% Identities = 89/173 (51%), Positives = 131/173 (75%) refINP_819272.1| ribosomal protein L10 [Coxiella burnetii RSA 493] gb|AAO89786.1| ribosomal protein L10 [Coxiella burnetii RSA 493] Length = 174

2108.2 Best-BlastP=>>nprot 45% Identities = 81/300 (27%), Positives = 142/300 (47%), Gaps = 14/300 (4%) refINP_561674.1| conserved hypothetical protein [Clostridium perfringens] dbj|BABB80464.1| conserved hypothetical protein [Clostridium perfringens str. 13] Length = 308

211.1 Best-BlastP=>>nprot 58% Identities = 118/341 (34%), Positives = 204/341 (59%), Gaps = 13/341 (3%) refINP_882114.1| putative membrane protein [Bordetella pertussis] refINP_882789.1| putative membrane protein [Bordetella parapertussis] refINP_886988.1| putative membrane protein [Bordetella bronchiseptica] emb|CAE43862.1| putative membrane protein [Bordetella pertussis] emb|CAE36021.1| putative membrane protein [Bordetella parapertussis] emb|CAE30937.1| putative membrane protein [Bordetella bronchiseptica] Length = 367

2112.2 Best-BlastP=>>nprot 28% Identities = 83/302 (27%), Positives = 137/302 (45%), Gaps = 15/302 (4%) refINP_772278.1| bll|5638 [Bradyrhizobium japonicum] dbj|BAC50903.1| bll|5638 [Bradyrhizobium japonicum USDA 110] Length = 500

2116.2 Best-BlastP=>>nprot 26% Identities = 23/73 (31%), Positives = 42/73 (57%), Gaps = 1/73 (1%) refINP_391095.1| transcriptional regulator [Bacillus subtilis] sp|P21340|PAIA_BACSU Protease synthase and sporulation negative regulatory protein PAI 1 emb|CAB15205.1| transcriptional regulator [Bacillus subtilis subsp. subtilis str. 168] Length = 172

2119.2 Best-BlastP=>>nprot 47% Identities = 175/527 (33%), Positives = 263/527 (49%), Gaps = 77/527 (14%) dbj|BAB86344.1| metalloprotease [Vibrio fluvialis] Length = 610

212.1 Best-BlastP=>>nprot 68% Identities = 83/152 (54%), Positives = 110/152 (72%), Gaps = 2/152 (1%) refINP_742683.1| phosphatidylglycerophosphatase A [Pseudomonas putida KT2440] gb|AAN66147.1|AE016242_15 phosphatidylglycerophosphatase A

2120.2 Best-BlastP=>>nprot No Hits found

2121.2 Best-BlastP=>>nprot 60% Identities = 108/221 (48%), Positives = 148/221 (66%), Gaps = 1/221 (0%) refINP_251544.1| conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir|B83288 conserved hypothetical protein PA2854 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06242.1|AE004712_2 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 323

2122.2 Best-BlastP=>>nprot 43% Identities = 100/377 (26%), Positives = 171/377 (45%), Gaps = 29/377 (7%) refINP_820237.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90751.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 408

2127.2 Best-BlastP=> >nrprot 62% Identities = 56/112 (50%), Positives = 74/112 (66%), Gaps = 3/112 (2%) ref|NP_840790.1| Uncharacterised protein family UPF0102 [Nitrosomonas europaea ATCC 19718] emb|CAD84622.1| Uncharacterised protein family UPF0102 [Nitrosomonas europaea ATCC 19718] Length = 118

2129.1 Best-BlastP=> >nrprot 70% Identities = 98/192 (51%), Positives = 141/192 (73%) ref|NP_743483.1| phosphoheptose isomerase [Pseudomonas putida KT2440] gb|AAN66947.1|AE016322_14 phosphoheptose isomerase [Pseudomonas putida KT2440] Length = 195

213.1 Best-BlastP=> >nrprot 56% Identities = 141/268 (52%), Positives = 180/268 (67%), Gaps = 4/268 (1%) ref|NP_406655.1| thiamine-monophosphate kinase [Yersinia pestis] ref|NP_668333.1| thiamin-monophosphate kinase [Yersinia pestis KIM] pir|AD0386 thiamine-monophosphate kinase (EC 2.7.4.16) [imported] - Yersinia pestis (strain CO92) emb|CAC92415.1| thiamine-monophosphate kinase [Yersinia pestis CO92] gb|AAM84584.1|AE013704_1 thiamin-monophosphate kinase [Yersinia pestis KIM] Length = 329

2130.1 Best-BlastP=> >nrprot 62% Identities = 88/188 (46%), Positives = 120/188 (63%), Gaps = 7/188 (3%) ref|NP_820724.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAQ91238.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 191

2132.2 Best-BlastP=> >nrprot 47% Identities = 53/181 (29%), Positives = 96/181 (53%), Gaps = 7/181 (3%) ref|NP_715937.1| lipoprotein, putative [Shewanella oneidensis MR-1] gb|AAN53382.1|AE015477_12 lipoprotein, putative [Shewanella oneidensis MR-1] Length = 188

2133.1 Best-BlastP=> >nrprot 53% Identities = 55/118 (46%), Positives = 70/118 (59%), Gaps = 1/118 (0%) ref|NP_254248.1| ATP synthase protein I [Pseudomonas aeruginosa PA01] pir|B82953 ATP synthase protein I PA5561 [imported] - Pseudomonas aeruginosa PAO1] Length = 126

2135.1 Best-BlastP=> >nrprot 53% Identities = 55/118 (46%), Positives = 70/118 (59%), Gaps = 1/118 (0%) ref|NP_254248.1| ATP synthase protein I [Pseudomonas aeruginosa PA01] pir|B82953 ATP synthase protein I PA5561 [imported] - Pseudomonas aeruginosa PAO1] Length = 126

2136.1 Best-BlastP=> >nrprot 75% Identities = 176/277 (63%), Positives = 210/277 (75%), Gaps = 19/277 (6%) ref|NP_720269.1| ATP synthase F0, A subunit [Shewanella oneidensis MR-1] gb|AAN57712.1|AE015907_10 ATP synthase F0, A subunit [Shewanella oneidensis MR-1] Length = 264

2137.1 Best-BlastP=> >nrprot 81% Identities = 72/80 (90%), Positives = 75/80 (93%) ref|ZP_00124678.1| COG0636: F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K [Pseudomonas syringae pv. syringae DC3000] gb|AAO59017.1| ATP synthase F0, C subunit [Pseudomonas syringae pv. tomato str. DC3000] Length = 85

2138.2 Best-BlastP=> >nrprot 72% Identities = 85/156 (54%), Positives = 114/156 (73%) ref|NP_820917.1| ATP synthase F0, B subunit [Coxiella burnetii RSA 493] gb|AAQ91431.1| ATP synthase F0, B subunit [Coxiella burnetii RSA 493] Length = 156

214.1 Best-BlastP=> >nrprot 66% Identities = 61/140 (43%), Positives = 99/140 (70%) ref|NP_252741.1| NusB protein [Pseudomonas aeruginosa PA01] sp|Q9HWX6|INUSB_PSEAE N utilization substance protein B homolog (NusB protein) pir|G83140 NusB protein PA4052 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07439.1|AE004821_12 NusB protein [Pseudomonas aeruginosa PAO1] Length = 159

2140.2 Best-BlastP=> >nrprot 64% Identities = 86/178 (48%), Positives = 116/178 (65%), Gaps = 2/178 (1%) ref|NP_254244.1| ATP synthase delta chain [Pseudomonas aeruginosa PA01] pir|F82952 ATP synthase delta chain PA5557 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAGG8942.1|AE004967_13 ATP synthase delta chain [Pseudomonas aeruginosa PAO1] Length = 178

2141.2 Best-BlastP=>>nrprot No Hits found

2143.5 Best-BlastP=>>nrprot 21% Identities = 66/242 (27%), Positives = 110/242 (45%), Gaps = 32/242 (13%) ref|NP_819452.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AO89966.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 262

2144.3 Best-BlastP=>>nrprot 59% Identities = 133/308 (43%), Positives = 196/308 (63%), Gaps = 1/308 (0%) ref|NP_716251.1| arginine N-succinyltransferase [Shewanella oneidensis MR-1] gb|AAN53696.1|AE015509_1 arginine N-succinyltransferase [Shewanella oneidensis MR-1] Length = 339

2146.2 Best-BlastP=>>nrprot 60% Identities = 151/363 (41%), Positives = 224/363 (61%), Gaps = 5/363 (1%) ref|NP_251855.1| histidinol-phosphate aminotransferase [Pseudomonas aeruginosa PA01] sp|Q9HZ68|H182_PSEAE Histidinol-phosphate aminotransferase 2 (Imidazole acetol-phosphate transaminase 2) pir|F83250 histidinol-phosphate aminotransferase PA3165 [imported] - Pseudomonas aeruginosa PAO1 Length = 369

2147.1 Best-BlastP=>>nrprot 70% Identities = 58/107 (54%), Positives = 80/107 (74%), Gaps = 2/107 (1%) ref|NP_840178.1| Pterin 4 alpha carbonylamine dehydratase [Nitrosomonas europaea] ATCC 19718] emb|CAD83988.1| Pterin 4 alpha carbonylamine dehydratase [Nitrosomonas europaea] ATCC 19718] Length = 113

2148.1 Best-BlastP=>>nrprot 75% Identities = 172/305 (56%), Positives = 230/305 (75%), Gaps = 1/305 (0%) ref|NP_820140.1| protein-export membrane protein SecF [Coxiella burnetii RSA 493] gb|AO90654.1| protein-export membrane protein SecF [Coxiella burnetii RSA 493] Length = 304

2149.4 Best-BlastP=>>nrprot 99% Identities = 427/431 (99%), Positives = 430/431 (99%) sp|Q8RNM2|PURA_LEGPN Adenylosuccinate synthetase (IMP--aspartate ligase) (AcSS) (AMPSase) gb|AM00648.1| adenylosuccinate synthetase [Legionella pneumophila] Length = 431

215.1 Best-BlastP=>>nrprot 79% Identities = 97/150 (64%), Positives = 124/150 (82%) ref|ZP_00126026.1| COG1327: Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-cone domains [Pseudomonas syringae pv. syringae B728a] Length = 165

2150.1 Best-BlastP=>>nrprot 39% Identities = 37/148 (25%), Positives = 64/148 (43%), Gaps = 19/148 (12%) ref|NP_799791.1| hypothetical protein VPA0281 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61624.1| hypothetical protein [Vibrio parahaemolyticus] Length = 133

2151.2 Best-BlastP=>>nrprot 14% Identities = 39/144 (27%), Positives = 67/144 (46%), Gaps = 24/144 (16%) sp|Q9U7E0|ATRX_CAEEL Transcriptional regulator ATRX homolog (X-linked nuclear protein-1) gb|AAD55361.1|AF134186_1 XNP-1 [Caenorhabditis elegans] = 1359

2152.2 Best-BlastP=>>nrprot 83% Identities = 127/176 (72%), Positives = 150/176 (85%) ref|NP_820460.1| antioxidant, AhpC/TSA family [Coxiella burnetii RSA 493] gb|AO90974.1| antioxidant, AhpC/TSA family [Coxiella burnetii RSA 493] Length = 179

2153.3 Best-BlastP=>>nrprot No Hits found

2156.3 Best-BlastP=>>nrprot 45% Identities = 126/444 (28%), Positives = 197/444 (44%), Gaps = 30/444 (6%) ref|NP_436941.1| putative oxidoreductase protein [Sinorhizobium meliloti] pir|A95892 probable oxidoreductase protein SmB20415 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb|CAC48801.1| putative oxidoreductase protein [Sinorhizobium meliloti] Length = 429

2159.2 Best-BlastP=>>nrprot 76% Identities = 163/238 (68%), Positives = 191/238 (80%) ref|NP_249464.1| pyridoxal phosphate biosynthetic protein PdxJ [Pseudomonas aeruginosa PA01] sp|Q915G5|PDXJ_PSEAE Pyridoxal phosphate biosynthetic protein PdxJ (PNP synthase) pir||H83548 pyridoxal phosphate biosynthetic protein PdxJ PA0773 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG04162.1|AE004512.5 pyridoxal phosphate biosynthetic protein PdxJ [Pseudomonas aeruginosa PAO1] Length = 248

216.2 Best-BlastP=>>nrprot 83% Identities = 296/416 (71%), Positives = 351/416 (84%), Gaps = 1/416 (0%) ref|ZP_00138159.1| COG0112: Glycine/serine hydroxymethyltransferase [Pseudomonas aeruginosa UCBPP-PA14] Length = 421

2160.2 Best-BlastP=>>nrprot 70% Identities = 166/329 (50%), Positives = 227/329 (68%), Gaps = 15/329 (4%) ref|NP_867540.1| 2-oxoglutarate ferredoxin oxidoreductase beta subunit [Pirellula sp.] emb|CAD75087.1| 2-oxoglutarate ferredoxin oxidoreductase beta subunit [Pirellula sp.] Length = 353

2162.2 Best-BlastP=>>nrprot 52% Identities = 153/496 (30%), Positives = 247/496 (49%), Gaps = 41/496 (8%) ref|NP_478172.1| amidase [Nostoc sp. PCC 7120] pir||AB2530 amidase [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120beta dbl|BAB77168.1| amidase [Nostoc sp. PCC 7120] Length = 507

2164.2 Best-BlastP=>>nrprot 48% Identities = 91/191 (47%), Positives = 135/191 (70%), Gaps = 1/191 (0%) ref|NP_820234.1| membrane protein, putative [Coxiella burnetii RSA 493] sp|Q83C89|YC39_COXBU Hypothetical UPF0078 protein CBU1239 gb|AAO90748.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 193

2166.2 Best-BlastP=>>nrprot No Hits found

2167.2 Best-BlastP=>>nrprot 65% Identities = 230/469 (49%), Positives = 315/469 (67%), Gaps = 5/469 (1%) ref|NP_819701.1| mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase [Coxiella burnetii RSA 493] gb|AAO90215.1| mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase [Coxiella burnetii RSA 493] Length = 477

2169.2 Best-BlastP=>>nrprot 69% Identities = 77/136 (56%), Positives = 95/136 (69%), Gaps = 4/136 (2%) ref|ZP_00067440.1| COG4969: Tfp pilus assembly protein, major pilin PilA [Microbulbifer degradans 2-40] Length = 164

2170.1 Best-BlastP=>>nrprot 60% Identities = 67/136 (49%), Positives = 84/136 (61%), Gaps = 5/136 (3%) ref|ZP_00067440.1| COG4969: Tfp pilus assembly protein, major pilin PilA [Microbulbifer degradans 2-40] Length = 164

2172.2 Best-BlastP=>>nrprot 52% Identities = 47/147 (31%), Positives = 81/147 (55%), Gaps = 1/147 (0%) ref|NP_717367.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN54811.1|AE015620_3 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 159

2173.2 Best-BlastP=>>nrprot 52% Identities = 59/125 (47%), Positives = 75/125 (60%), Gaps = 1/125 (0%) sp|Q45292|YQUG_BACLI Hypothetical 17.3 kDa protein in GNTR 5'region pir||JC2302 oug protein - Bacillus licheniformis dbl|BAA06500.1| hypothetical protein [Bacillus licheniformis] Length = 147

2174.1 Best-BlastP=>>nrprot 50% Identities = 37/71 (52%), Positives = 50/71 (70%) ref|NP_840482.1| DUF167 [Nitrosomonas europaea ATCC 19718] emb|CAD84306.1| DUF167 [Nitrosomonas europaea ATCC 19718] Length = 100

2175.3 Best-BlastP=>>nrprot No Hits found

2176.3 Best-BlastP=>>nrprot 52% Identities = 35/119 (29%), Positives = 64/119 (53%), Gaps = 6/119 (5%) ref|NP_784901.1| unknown [Lactobacillus plantarum WCF51] emb|CAD63748.1| unknown [lactobacillus plantarum WCF51] Length = 269

2177.2 Best-BlastP=>>nrprot 53% Identities = 71/181 (39%), Positives = 104/181 (57%), Gaps = 1/181 (0%) ref|ZP_00052983.1| COG0582: Integrase [Magnetospirillum magnetotacticum] Length = 193

2180.2 Best-BlastP=>>nrprot 19% Identities = 68/171 (39%), Positives = 95/171 (55%), Gaps = 5/171 (2%) ref|NP_814807.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] gb|AAO80877.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] Length = 168

2188.2 Best-BlastP=>>nrprot 45% Identities = 64/241 (26%), Positives = 113/241 (46%), Gaps = 17/241 (7%) ref|NP_719332.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56776.1|AE015813_4 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 250

2191.4 Best-BlastP=>>nrprot 74% Identities = 88/168 (52%), Positives = 127/168 (75%) ref|NP_709074.1| peptide deformylase [Shigella flexneri 2a str. 301] ref|NP_838779.1| peptide deformylase [Shigella flexneri 2a str. 2457T] gb|AAN44781.1|AE015342_8 peptide deformylase [Shigella flexneri 2a str. 301] gb|AAP18590.1| peptide deformylase [Shigella flexneri 2a str. 2457T] Length = 169

2193.4 Best-BlastP=>>nrprot 90% Identities = 33/419 (78%), Positives = 379/419 (90%) dbj|BAC95945.1| transcription termination factor [Vibrio vulnificus YJ016] Length = 427

2195.1 Best-BlastP=>>nrprot 84% Identities = 356/487 (73%), Positives = 415/487 (85%) ref|NP_667799.1| putative oxidoreductase [Yersinia pestis KIM] gb|AAM84050.1|AE013646_10 putative oxidoreductase [Yersinia pestis KIM] Length = 506

2196.1 Best-BlastP=>>nrprot 51% Identities = 77/233 (33%), Positives = 122/233 (52%), Gaps = 11/233 (4%) ref|NP_903454.1| NAD(P)H-flavin reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ61446.1| NAD(P)H-flavin reductase [Chromobacterium violaceum ATCC 12472] Length = 342

2197.1 Best-BlastP=>>nrprot No Hits found

2198.1 Best-BlastP=>>nrprot 55% Identities = 35/104 (33%), Positives = 58/104 (55%), Gaps = 4/104 (3%) ref|ZP_00012205.1| COG3785: Uncharacterized conserved protein [Rhodopseudomonas palustris] Length = 110

2199.2 Best-BlastP=>>nrprot 97% Identities = 235/238 (98%), Positives = 236/238 (99%) emb|CAC34416.1| putative TatC protein [Legionella pneumophila] Length = 238

220.1 Best-BlastP=>>nrprot 65% Identities = 123/228 (53%), Positives = 152/228 (66%) ref|NP_819791.1| glutamine amidotransferase, class I [Coxiella burnetii RSA 493] gb|AAO90305.1| glutamine amidotransferase, class I [Coxiella burnetii RSA 493] Length = 228

2204.2 Best-BlastP=>>nrprot 72% Identities = 279/498 (56%), Positives = 369/498 (74%), Gaps = 3/498 (0%) ref|NP_841949.1| Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb|CAD85838.1| Sulfate transporter [Nitrosomonas europaea ATCC 19718] Length = 539

2207.2 Best-BlastP=>>nrprot 79% Identities = 126/208 (60%), Positives = 167/208 (80%) ref|NP_841948.1| Prokaryotic-type carbonic anhydrase [Nitrosomonas europaea ATCC 19718] emb|CAD85837.1| Prokaryotic-type carbonic anhydrase [Nitrosomonas europaea ATCC 19718] Length = 208

2208.1 Best-BlastP=>>nrprot No Hits found

2209.4 Best-BlastP=>>nrprot 58% Identities = 111/321 (34%), Positives = 189/321 (58%), Gaps = 7/321 (2%) ref|NP_814373.1| ornithine cyclodeaminase, putative [Enterococcus faecalis V583] gb|AAM75325.1|AF454824_124 EF0124 [Enterococcus faecalis] gb|AAO80444.1| ornithine cyclodeaminase, putative [Enterococcus faecalis V583] Length = 326

221.1 Best-BlastP=>>nrprot 70% Identities = 158/285 (55%), Positives = 212/285 (74%) ref|ZP_00033588.1| COG0329: Dihydrodipicolinate synthase/N-acetylneuraminate lyase [Burkholderia fungorum] Length = 297

2212.4 Best-BlastP=>>nrprot 51% Identities = 232/616 (37%), Positives = 344/616 (55%), Gaps = 48/616 (7%) ref|NP_762611.1| Type IV secretory pathway, VirD4 component [Vibrio vulnificus CMCP6] gb|AAO07601.1|AE016810_104 Type IV secretory pathway, VirD4 component [Vibrio vulnificus CMCP6] Length = 697

2213.2 Best-BlastP=>>nrprot No Hits found

2217.3 Best-BlastP=>>nrprot 66% Identities = 302/609 (49%), Positives = 411/609 (67%), Gaps = 13/609 (2%) sp|P32966|UVRC_PSEFL Excinuclease ABC subunit C gb|AAQ98758.1| UVR excinuclease subunit C Length = 607

2219.2 Best-BlastP=>>nrprot 34% Identities = 41/91 (45%), Positives = 48/91 (52%) gb|AAA73346.1| [Mycobacterium tuberculosis DNA sequence, complete cds.], gene products Length = 152

222.1 Best-BlastP=>>nrprot 63% Identities = 73/149 (48%), Positives = 102/149 (68%), Gaps = 5/149 (3%) ref|NP_928633.1| hypothetical protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE13616.1| unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] Length = 149

2220.2 Best-BlastP=>>nrprot 71% Identities = 110/213 (51%), Positives = 156/213 (73%) ref|NP_486035.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AE2055 hypothetical protein all1995 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB73694.1| ORF_ID:all1995~hypothetical protein [Nostoc sp. PCC 7120] Length = 221

2221.3 Best-BlastP=>>nrprot 57% Identities = 58/132 (43%), Positives = 84/132 (63%), Gaps = 4/132 (3%) gb|EAA20351.1| cytosol aminopeptidase [Plasmidum yoelii yoelii] Length = 612

2225.2 Best-BlastP=>>nrprot 55% Identities = 116/284 (40%), Positives = 167/284 (58%), Gaps = 6/284 (2%) ref|NP_9023861.1| geranyltranstransferase [Chromobacterium violaceum ATCC 12472] gb|AAQ60361.1| geranyltranstransferase [Chromobacterium violaceum ATCC 12472] Length = 298

223.1 Best-BlastP=>>nrprot 51% Identities = 97/266 (36%), Positives = 151/266 (56%), Gaps = 9/266 (3%) ref|ZP_00020713.1| hypothetical protein [Chloroflexus aurantiacus] Length = 278

2230.2 Best-BlastP=>>nrprot 58% Identities = 68/196 (34%), Positives = 117/196 (59%), Gaps = 2/196 (1%) ref|NP_767278.1| Maf-like protein [Bradyrhizobium japonicum] dbj|BAC45903.1| Maf-like protein [Bradyrhizobium japonicum USDA 110] Length = 202

2231.3 Best-BlastP=>>nrprot 75% Identities = 254/407 (62%), Positives = 318/407 (78%), Gaps = 1/407 (0%) ref|ZP_00079853.1| COG0148: Endolase [Geobacter metallireducens] Length = 429

2232.1 Best-BlastP=>>nrprot 32% Identities = 41/123 (33%), Positives = 61/123 (49%), Gaps = 5/123 (4%) ref|NP_899813.1| 2-dehydro-3-deoxy-phosphogluconate aldolase [Chromobacterium violaceum ATCC 12472] Length = 208

2233.3 Best-BlastP=>>nrprot 63% Identities = 64/119 (53%), Positives = 83/119 (69%) ref|NP_819436.1| lipoprotein signal peptidase [Coxiella burnetii RSA 493] Length = 163

2235.2 Best-BlastP=>>nrprot 57% Identities = 220/636 (34%), Positives = 371/636 (58%), Gaps = 29/636 (4%) ref|NP_819137.1| sulfatase domain protein [Coxiella burnetii RSA 493] gb|AAO89651.1| sulfatase domain protein [Coxiella burnetii RSA 493] Length = 638

2239.3 Best-BlastP=>>nrprot 45% Identities = 96/277 (34%), Positives = 149/277 (53%), Gaps = 40/277 (14%) emb|CAA75849.1| hypothetical protein [Coxiella burnetii] Length = 309

2240.2 Best-BlastP=>>nrprot 66% Identities = 75/155 (48%), Positives = 105/155 (67%) ref|ZP_00067293.1| COG1576: Uncharacterized conserved protein [Microbulbifer degradans] Length = 155

2241.2 Best-BlastP=>>nrprot 67% Identities = 51/105 (48%), Positives = 76/105 (72%) ref|ZP_00090593.1| COG0799: Uncharacterized homolog of plant lojap protein Length = 117
[Azotobacter vinelandii]

2242.1 Best-BlastP=>>nrprot 47% Identities = 46/187 (24%), Positives = 89/187 (47%), Gaps = 16/187 (8%) ref|NP_820065.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90579.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 184

2244.2 Best-BlastP=>>nrprot 77% Identities = 129/202 (63%), Positives = 156/202 (77%) gb|AAC33273.1| TnpR [Pseudomonas alcaligenes]

Length = 309

2245.2 Best-BlastP=>>nrprot 65% Identities = 178/331 (53%), Positives = 236/331 (71%), Gaps = 6/331 (1%) ref|NP_842305.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 346

2247.5 Best-BlastP=>>nrprot 61% Identities = 233/551 (42%), Positives = 342/551 (62%), Gaps = 4/551 (0%) ref|NP_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAI02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589

2250.2 Best-BlastP=>>nrprot No Hits found

2251.3 Best-BlastP=>>nrprot No Hits found

2252.1 Best-BlastP=>>nrprot 83% Identities = 254/363 (69%), Positives = 303/363 (83%) ref|NP_231816.1| GTP-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|D82107 GTP-binding protein VC2185 [imported] - Vibrio cholerae (strain gb|AAF95330.1|) GTP-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 383

2253.2 Best-BlastP=>>nrprot 66% Identities = 96/181 (53%), Positives = 127/181 (70%) ref|NP_283782.1| putative peptidyl-tRNA hydrolase [Neisseria meningitidis Z2491] sp|Q9JV42|PTH_NEIMA Peptidyl-tRNA hydrolase (PTH) pir|B81948 probable aminoacyl-tRNA hydrolase (EC 3.1.1.29) NMA1004 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) embl|CAB84273.1| putative peptidyl-tRNA hydrolase [Neisseria meningitidis Z2491] Length = 192

2255.2 Best-BlastP=>>nrprot 67% Identities = 158/294 (53%), Positives = 199/294 (67%), Gaps = 4/294 (1%) ref|NP_461016.1| ATP phosphoribosyltransferase [Salmonella typhimurium LT2] sp|P00499|HS1_SALTY ATP phosphoribosyltransferase pir|XREBT ATP phosphoribosyltransferase (EC 2.4.2.17) [validated] - Salmonella typhimurium emb|CAA31822.1| unnamed protein product [Salmonella typhimurium] gb|AAA27142.1| hisG gb|AA88614.1| ATP phosphoribosyltransferase gb|AA80244.1| ATP phosphoribosyltransferase gb|AA80247.1| ATP phosphoribosyltransferase gb|AA80249.1| ATP phosphoribosyltransferase gb|AA80252.1| ATP phosphoribosyltransferase gb|AA80257.1| ATP phosphoribosyltransferase gb|AA80259.1| ATP phosphoribosyltransferase gb|AA80262.1| ATP phosphoribosyltransferase gb|AA80267.1| ATP phosphoribosyltransferase [Salmonella typhimurium LT2] Length = 299

2258.2 Best-BlastP=>>nrprot No Hits found

226.4 Best-BlastP=>>nrprot No Hits found

2260.2 Best-BlastP=>>nrprot 65% Identities = 115/209 (55%), Positives = 147/209 (70%), Gaps = 1/209 (0%) ref|ZP_00013996.1| COG2872: Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain [Rhodospirillum rubrum] Length = 214

2261.3 Best-BlastP=>>nrprot No Hits found

2264.2 Best-BlastP=>>nrprot 59% Identities = 172/411 (41%), Positives = 247/411 (60%), Gaps = 6/411 (1%) ref|NP_773878.1| b|r7238 [Bradyrhizobium japonicum] dbj|BAC52503.1| b|r7238 [Bradyrhizobium japonicum USDA 110] Length = 412

2266.2 Best-BlastP=>>nrprot 76% Identities = 282/410 (68%), Positives = 322/410 (78%), Gaps = 1/410 (0%) ref|ZP_00021755.1| hypothetical protein [Ralstonia metallidurans]

2268.2 Best-BlastP=>>nrprot 48% Identities = 131/405 (32%), Positives = 197/405 (48%), Gaps = 29/405 (7%) ref|NP_616925.1| conserved hypothetical protein [Methanosa sarcina acetylavorans str. C2A] gb|AAM05405.1| conserved hypothetical protein [Methanosa sarcina acetylavorans str. C2A] Length = 417

227.2 Best-BlastP=>>nrprot 95% Identities = 281/303 (92%), Positives = 291/303 (96%) gb|AAM00625.1| unknown [Legionella pneumophila] Length = 303

2270.2 Best-BlastP=>>nrprot 45% Identities = 38/120 (31%), Positives = 58/120 (48%), Gaps = 22/120 (18%) gb|AAA89101.1| protein kinase Length = 379

2271.1 Best-BlastP=>>nrprot 41% Identities = 25/57 (43%), Positives = 35/57 (61%), Gaps = 4/57 (7%) ref|NP_012348.1| Delays the onset of mitosis by phosphorylation and inactivation of the cyclin-dependent kinase Cdc28, thereby relaying the morphogenetic signal to the cell cycle. S. pombe wee1+ homolog; Swe1p [Saccharomyces cerevisiae] sp|P32944|SWE1 YEAST Mitosis inhibitor protein kinase SWE1 [S40400 protein kinase SWE1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)] embl|CAA52150.1| SWE1 [Saccharomyces cerevisiae] Length = 819

2272.3 Best-BlastP=>>nrprot 61% Identities = 228/487 (46%), Positives = 308/487 (63%), Gaps = 8/487 (1%) ref|NP_744150.1| amidophosphoribosyltransferase [Pseudomonas putida KT2440] gb|AAN67614.1|AE016391_5 amidophosphoribosyltransferase [Pseudomonas putida KT2440] Length = 501

2274.2 Best-BlastP=>>nrprot 74% Identities = 194/313 (61%), Positives = 233/313 (74%), Gaps = 5/313 (1%) gb|AAL85973.1| putative phosphoribosyamidoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] Length = 374

2275.3 Best-BlastP=>>nrprot 34% Identities = 75/185 (40%), Positives = 107/185 (57%), Gaps = 19/185 (10%) ref|NP_437235.1| putative protein, similar to gene related to biosynthesis of peptide antibiotic trifolitoxin [Sinorhizobium meliloti] pirl|G95928 hypothetical protein SMb21116 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB embl|CAC49095.1| putative protein, similar to gene related to biosynthesis of peptide antibiotic trifolitoxin [Sinorhizobium meliloti] Length = 243

2277.2 Best-BlastP=>>nrprot 47% Identities = 27/55 (49%), Positives = 41/55 (74%), Gaps = 1/55 (1%) ref|NP_820051.1| carbon storage regulator [Coxiella burnetii RSA 493] gb|AO90565.1| carbon storage regulator [Coxiella burnetii RSA 493] Length = 70

2279.2 Best-BlastP=>>nrprot No Hits found

228.1 Best-BlastP=>>nrprot No Hits found

2282.4 Best-BlastP=>>nrprot 98% Identities = 569/577 (98%), Positives = 571/577 (98%), Gaps = 1/577 (0%) sp|P71481|PRIM_LEGPN DNA primase gb|AB09542.1| LpdnaG Length = 576

2289.2 Best-BlastP=>>nrprot 50% Identities = 50/159 (31%), Positives = 81/159 (50%), Gaps = 13/159 (8%) ref|NP_718655.1| hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56099.1|AE015746_3 hypothetical protein [Shewanella oneidensis MR-1] Length = 197

2290.1 Best-BlastP=>>nrprot 53% Identities = 106/293 (36%), Positives = 164/293 (55%), Gaps = 2/293 (0%) ref|NP_744181.1| conserved hypothetical protein [Pseudomonas putida KT2440] gb|AAN67645.1|AE016394_6 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 318

2291.2 Best-BlastP=>>nrprot 81% like ATPases [Microbulbifer degradans 2-40] Identities = 208/316 (65%), Positives = 262/316 (82%), Gaps = 1/316 (0%) ref|ZP_00067583.1| COG0714; MoxR chain Length = 321

2292.2 Best-BlastP=>>nrprot 28% Identities = 81/371 (21%), Positives = 158/371 (42%), Gaps = 34/371 (9%) pir|[2210342A myosin:SUBUNIT=heavy chain Length = 2241

2293.5 Best-BlastP=>>nrprot 14% protein [Bacillus anthracis str. Ames] gb|AAP26124.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 324

2295.3 Best-BlastP=>>nrprot 72% [Pseudomonas aeruginosa PA01] pir|[A83520 bacterioferritin comigratory protein PA1008 [imported] - PAO1] db|AG04397.1|AE004533_8 bacterioferritin comigratory protein [Pseudomonas aeruginosa PAO1] Length = 157

2297.3 Best-BlastP=>>nrprot 79% [Escherichia coli O157:H7] ref|NP_417110.1| small protein B [Escherichia coli K12] ref|NP_708467.1| small protein B [Shigella flexneri 2a str. 301] ref|NP_755024.1| SsrA-binding protein [Escherichia coli CFT073] ref|NP_838189.1| ssrA(tmRNA)-binding protein [Shigella flexneri 2a str. 2457T] sp|P32052|SSRP_ECOLI_SsrA-binding protein (Small protein B) pir|[JS0701 small protein B, smpB - Escherichia coli (strain K-12) pir|B91064 small protein B [imported] - Escherichia coli (strain O157:H7, substring RIMD 0509952) dbj|BAA02062.1| small protein [Escherichia coli] gb|AAJ79790.1| smpB gene product gb|AAC75669.1| small protein B [Escherichia coli K12] dbj|BAB36905.1| small protein B [Escherichia coli O157:H7] gb|AAN44174.1|AE015283_5 small protein B [Shigella flexneri 2a str. 301] gb|AN81592.1|AE016764_274_SsrA-binding protein [Escherichia coli CFT073] gb|AAP17999.1| ssrA(tmRNA)-binding protein [Shigella flexneri 2a str. 2457T] Length = 160

2298.2 Best-BlastP=>>nrprot 16% Identities = 40/142 (28%), Positives = 73/142 (51%), Gaps = 8/142 (5%) ref|NP_038716.1| t-complex-associated testis expressed 1 [Mus musculus] pir|[A45841 T-complex-associated-testes-expressed-1 protein - mouse gb|AAA40406.1| Tcte-1 peptide Length = 506

2299.3 Best-BlastP=>>nrprot 37% Identities = 22/88 (25%), Positives = 41/88 (46%), Gaps = 5/88 (5%) ref|NP_819930.1| conserved domain protein [Coxiella burnetii RSA 493] gb|AAO90444.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 169

2301.2 Best-BlastP=>>nrprot 70% [Coxiella burnetii RSA 493] gb|AAO90604.1| ribonuclease R [Coxiella burnetii RSA 493] Length = 736

2302.2 Best-BlastP=>>nrprot 72% [Coxiella burnetii RSA 493] gb|AAK87951.1| AGR_C_4014p [Agrobacterium tumefaciens] ref|NP_532881.1| secretion chaperone [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|[F97624 csaa protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK87951.1| AGR_C_4014p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL43197.1| secretion chaperone [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 113

2308.2 Best-BlastP=>>nrprot No Hits found

2309.2 Best-BlastP=>>nrprot 45% Identities = 104/406 (25%), Positives = 173/406 (42%), Gaps = 63/406 (15%) sp|Q9MYU4|ENP1_PIG Ectonucleoside triphosphate diphosphohydrolase 1 (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) [Lymphoid cell activation antigen] (Ecto-apyrase) (CD39 antigen) emb|CAB95871.1| ATP-diphosphohydrolase [Sus scrofa] Length = 510

2311.4 Best-BlastP=>>nrprot 75% Identities = 490/868 (56%), Positives = 648/868 (74%), Gaps = 13/868 (1%) ref|NP_928561.1| alanyl-tRNA synthetase (alanine-tRNA ligase) [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE13544.1| alanyl-tRNA synthetase (alanine-tRNA ligase) [Photorhabdus luminescens subsp. laumontii TTO1] Length = 876

2312.1 Best-BlastP=>>nrprot No Hits found

2313.2 Best-BlastP=>>nrprot 19% Identities = 40/156 (25%), Positives = 78/156 (50%), Gaps = 13/156 (8%) ref|NP_614055.1| Uncharacterized protein [Methanopyrus kandleri AV19] gbl|AAM01985.1| Uncharacterized protein [Methanopyrus kandleri AV19] Length = 609

2315.3 Best-BlastP=>>nrprot 56% Identities = 93/262 (35%), Positives = 149/262 (56%), Gaps = 2/262 (0%) ref|ZP_00108734.1| COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Nostoc punctiforme] Length = 270

2317.2 Best-BlastP=>>nrprot 71% Identities = 266/484 (54%), Positives = 351/484 (72%), Gaps = 1/484 (0%) ref|NP_390984.1| glycine betaine aldehyde dehydrogenase [Bacillus subtilis] sp|P71016|DHAB_BACSU Betaine aldehyde dehydrogenase (BADH) pir|A69629 glycine betaine aldehyde dehydrogenase gbsA - Bacillus subtilis gbl|AAC44364.1| GbsA emb|CAB15084.1| glycine betaine aldehyde dehydrogenase [Bacillus subtilis subsp. subtilis str. 168] Length = 490

2319.3 Best-BlastP=>>nrprot 72% Identities = 263/462 (56%), Positives = 331/462 (71%), Gaps = 6/462 (1%) ref|NP_638201.1| L-serine dehydratase [Xanthomonas campestris pv. campestris str. ATCC 33913] gbl|AAM42125.1| L-serine dehydratase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 460

2320.3 Best-BlastP=>>nrprot 50% Identities = 163/400 (40%), Positives = 243/400 (60%), Gaps = 17/400 (4%) ref|NP_865739.1| alginic o-acetyltransferase algI [Pirellula sp.] emb|CAD73424.1| alginic o-acetyltransferase algI [Pirellula sp.] Length = 470

2321.3 Best-BlastP=>>nrprot 65% Identities = 90/172 (52%), Positives = 120/172 (69%) ref|NP_884513.1| putative chromate reductase [Bordetella parapertussis] ref|NP_88264.1| putative chromate reductase [Bordetella bronchiseptica] emb|CAE32216.1| putative chromate reductase [Bordetella bronchiseptica] emb|CAE37565.1| putative chromate reductase [Bordetella parapertussis] Length = 184

2322.2 Best-BlastP=>>nrprot 65% Identities = 113/231 (48%), Positives = 152/231 (65%), Gaps = 3/231 (1%) ref|NP_820714.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gbl|AAO91228.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 237

2323.2 Best-BlastP=>>nrprot 34% Identities = 47/220 (21%), Positives = 91/220 (41%), Gaps = 16/220 (7%) ref|NP_902123.1| hypothetical protein Cv2453 [Chromobacterium violaceum ATCC 12472] gbl|AAQ60124.1| hypothetical protein CV2453 [Chromobacterium violaceum ATCC 12472] Length = 258

2324.4 Best-BlastP=>>nrprot No Hits found

2328.2 Best-BlastP=>>nrprot 61% Identities = 376/865 (43%), Positives = 527/865 (60%), Gaps = 23/865 (2%) ref|NP_778639.1| diaminopimelate decarboxylase; aspartate kinase [Xylella fastidiosa] gbl|AO28288.1| diaminopimelate decarboxylase; aspartate kinase [Xylella fastidiosa] Temecula1 Length = 868

2330.2 Best-BlastP=>>nprot 72% Identities = 380/665 (57%), Positives = 488/665 (73%), Gaps = 1/665 (0%) ref|NP_246655.1| Lig [Pasteurella multocida] gbl|AAK03800_1| Lig [Pasteurella multocida] Length = 673

2333.3 Best-BlastP=>>nprot 70% Identities = 381/700 (54%), Positives = 501/700 (71%), Gaps = 10/700 (1%) ref|NP_841209.1| Bacterial extracellular solute-binding protein, family 5 [Nitrosomonas europaea ATCC 19718] emb|CAD85063.1| Bacterial extracellular solute-binding protein, family 5 [Nitrosomonas europaea ATCC 19718] Length = 746

2335.2 Best-BlastP=>>nprot No Hits found

2336.2 Best-BlastP=>>nprot 70% Identities = 353/672 (52%), Positives = 479/672 (71%), Gaps = 4/672 (0%) ref|NP_796449.1| oligopeptidase A [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC583333.1| oligopeptidase A [Vibrio parahaemolyticus] Length = 680

2337.3 Best-BlastP=>>nprot 76% Identities = 135/215 (62%), Positives = 170/215 (79%) gbl|AAK20881.1|AF334761_2 cell division ATP-binding protein [Aeromonas hydrophila] Length = 222

2339.4 Best-BlastP=>>nprot 74% Identities = 210/345 (60%), Positives = 264/345 (76%), Gaps = 6/345 (1%) ref|ZP_00126801.1| COG0552: Signal recognition particle GTPase [Pseudomonas syringae] pv. syringae B728a] Length = 505

234.2 Best-BlastP=>>nprot 99% Identities = 731/736 (99%), Positives = 734/736 (99%) gbl|AAM00624.1| putative copper efflux ATPase [Legionella pneumophila] Length = 736

2343.2 Best-BlastP=>>nprot 33% Identities = 67/259 (25%), Positives = 108/259 (41%), Gaps = 34/259 (13%) ref|NP_359656.1| cell surface antigen [Rickettsia conorii] pir|C97702 cell surface antigen [imported] - Rickettsia conorii (strain Malish) Length = 1902

2344.4 Best-BlastP=>>nprot 56% Identities = 270/726 (37%), Positives = 405/726 (55%), Gaps = 16/726 (2%) ref|ZP_00043557.1| COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1] Length = 734

2345.2 Best-BlastP=>>nprot No Hits found

2346.1 Best-BlastP=>>nprot No Hits found

2347.2 Best-BlastP=>>nprot No Hits found

235.2 Best-BlastP=>>nprot 50% Identities = 145/450 (32%), Positives = 218/450 (48%), Gaps = 60/450 (13%) sp|P42042|AMYG_ARXAD Glucoamylase precursor (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) emb|CAA86997.1| glucoamylase precursor [Arxula adeninivorans] Length = 624

2350.2 Best-BlastP=>>nprot No Hits found

2351.2 Best-BlastP=>>nprot 59% Identities = 114/258 (44%), Positives = 164/258 (63%) ref|ZP_00122702.1| COG1043: Acyl-[acyl carrier protein]-O-acyltransferase [Haemophilus somnis 129PT] Length = 262

2352.2 Best-BlastP=>>nprot 66% Identities = 229/338 (67%) ref|ZP_00052962.1| COG1044: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Magnetospirillum magnetotacticum] Length = 339

2353.3 Best-BlastP=>>nprot 65% Identities = 174/375 (46%), Positives = 251/375 (66%), Gaps = 3/375 (0%) ref|NP_252333.1| lipid A-disaccharide synthase [Pseudomonas aeruginosa PA01] sp|Q9HXY8|LPXB_PSEAE Lipid-A-disaccharide synthase pir|C83190 lipid A-disaccharide synthase PA3643 [imported] - Pseudomonas aeruginosa (strain PAO1) gbl|AAQ07031.1|AE004784_4 lipid A-disaccharide synthase [Pseudomonas aeruginosa PAO1] Length = 378

2354.2 Best-BlastP=>>nrprot 23% *Vibrio vulnificus* YJ016] Identities = 27/92 (29%), Positives = 49/92 (53%), Gaps = 2/92 (2%) *dbj|BAC97056.1| RTX* (repeat in toxin) cytotoxin Length = 5206

2355.2 Best-BlastP=>>nrprot 45% *Vibrio vulnificus* YJ016] Identities = 83/256 (32%), Positives = 134/256 (52%), Gaps = 18/256 (7%) *ref|NP_832533.1| Probable short-chain type dehydrogenase/reductase* *vdIC* [Bacillus cereus ATCC 14579] *gb|AAP09734.1| Probable short-chain type dehydrogenase/reductase* Length = 281

2356.2 Best-BlastP=>>nrprot 65% *Vibrio vulnificus* YJ016] Identities = 106/213 (49%), Positives = 141/213 (66%), Gaps = 2/213 (0%) *ref|ZP_00138632.1| COG0259: Pyridoxamine-phosphate oxidase* [Pseudomonas aeruginosa UCBPP-PA14] Length = 215

2357.4 Best-BlastP=>>nrprot 6% *Escherichia coli* CFT073] *gb|AAN79355.1|AE016757_259* Putative conserved protein [Escherichia coli CFT073] Length = 101

2358.3 Best-BlastP=>>nrprot 73% *Escherichia coli* CFT073] *gb|AAN79355.1|AE016757_259* Putative conserved protein [Escherichia coli CFT073] Length = 101

236.1 Best-BlastP=>>nrprot No Hits found

2360.2 Best-BlastP=>>nrprot 52% *Nostoc* sp. *PCC 7120*] *pir|AE2105* hypothetical protein *all2396* [imported] - *Nostoc* sp. (strain *PCC 7120*) *dbj|BAB74095.1| ORF_ID* *all2396*-unknown protein [Nostoc sp. *PCC 7120*] Length = 454

2361.4 Best-BlastP=>>nrprot 21% *Dictyostelium discoideum*] *gb|AAC34582.1| interaptin* [Dictyostelium discoideum] *Length = 1738*

2362.3 Best-BlastP=>>nrprot 99% *Dictyostelium discoideum*] *gb|AAC34582.1| interaptin* [Dictyostelium discoideum] *Length = 1738*

2364.1 Best-BlastP=>>nrprot 99% *Dictyostelium discoideum*] *gb|AAC38180.1| DotC* [Legionella pneumophila] *Length = 303*

2365.2 Best-BlastP=>>nrprot 52% *Legionella pneumophila*] *Length = 377*

2368.5 Best-BlastP=>>nrprot 46% *Legionella pneumophila*] *Length = 377*

2369.3 Best-BlastP=>>nrprot 54% *Pseudomonas putida* KT2440] *gb|AAN66541.1|AE016282_9* transporter, LysE family *[Pseudomonas putida* KT2440] *Length = 204*

2371.1 Best-BlastP=>>nrprot 51% *Pseudomonas putida* KT2440] *gb|AAN66541.1|AE016282_9* transporter, LysE family *[Pseudomonas putida* KT2440] *Length = 204*

2371.1 Best-BlastP=>>nrprot 51% *Streptomyces avermitilis* MA-4680] *dbj|BAC68086.1| putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase* *[Streptomyces avermitilis* MA-4680] *Length = 495*

2371.1 Best-BlastP=>>nrprot 51% *Streptomyces avermitilis* MA-4680] *Length = 495*

2371.1 Best-BlastP=>>nrprot 51% *Rickettsia conorii*] *pir|G97771 capM* protein [imported] - *Rickettsia conorii* (strain Malish 7) *gb|AAL03113.1| capM* protein [Rickettsia conorii] *Length = 338*

2372.3 Best-BlastP=>>nrprot 66% Identities = 53/118 (44%), Positives = 79/118 (66%) ref|ZP_00111665.1| COG2146: Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases [Nostoc punctiforme] Length = 119

2373.2 Best-BlastP=>>nrprot 73% Identities = 185/309 (59%), Positives = 235/309 (76%), Gaps = 2/309 (0%) ref|NP_819938.1| lytic murein transglycosylase, putative [Coxiella burnetii RSA 493] gb|AAO90452.1| lytic murein transglycosylase, putative [Coxiella burnetii RSA 493] Length = 333

2374.2 Best-BlastP=>>nrprot No Hits found

2375.3 Best-BlastP=>>nrprot 75% Identities = 115/187 (61%), Positives = 144/187 (77%), Gaps = 2/187 (1%) ref|ZP_00091537.1| COG0164: Ribonuclease HII [Azotobacter vinelandii] Length = 236

2377.2 Best-BlastP=>>nrprot 73% Identities = 181/309 (58%), Positives = 236/309 (76%) ref|NP_819651.1| oxidoreductase family protein [Coxiella burnetii RSA 493] gb|AAO90165.1| oxidoreductase family protein [Coxiella burnetii RSA 493] Length = 327

238.1 Best-BlastP=>>nrprot 57% Identities = 185/432 (42%), Positives = 272/432 (62%), Gaps = 10/432 (2%) ref|NP_391464.1| similar to metabolite transport protein [Bacillus subtilis] pir|E70070 metabolite transport protein homolog ywtG - Bacillus subtilis emb|CAB07473.1| ywtG [Bacillus subtilis] Length = 457

2381.2 Best-BlastP=>>nrprot 58% Identities = 148/381 (38%), Positives = 225/381 (59%), Gaps = 2/381 (0%) ref|ZP_00079875.1| COG0763: Lipid A disaccharide synthetase [Geobacter metallireducens] Length = 400

2382.2 Best-BlastP=>>nrprot 54% Identities = 39/79 (49%), Positives = 54/79 (68%) ref|NP_716031.1| DNA-binding protein Fis [Shewanella oneidensis MR-1] gb|AAN53476.1|AE015487_10 DNA-binding protein Fis [Shewanella oneidensis MR-1] Length = 101

2383.4 Best-BlastP=>>nrprot 37% Identities = 21/45 (46%), Positives = 26/45 (57%), Gaps = 2/45 (4%) gb|AAQ17065.1| nucleolin 3 [Cyprinus carpio] gb|AAQ55855.1| nucleolin [Cyprinus carpio] Length = 637

2387.3 Best-BlastP=>>nrprot 55% Identities = 130/320 (40%), Positives = 187/320 (58%), Gaps = 4/320 (1%) ref|NP_768143.1| quinone oxidoreductase [Bradyrhizobium japonicum] dbj|BAC46768.1| quinone oxidoreductase [Bradyrhizobium japonicum USDA 110] Length = 332

2388.3 Best-BlastP=>>nrprot 72% Identities = 147/280 (52%), Positives = 212/280 (75%) ref|ZP_00021514.1| COG1175: ABC-type sugar transport systems, permease components [Ralstonia metallidurans] Length = 293

239.1 Best-BlastP=>>nrprot 65% Identities = 106/203 (52%), Positives = 145/203 (71%) ref|NP_718073.1| 2-deydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate Length = 213

2391.2 Best-BlastP=>>nrprot No Hits found

2392.2 Best-BlastP=>>nrprot No Hits found

2395.3 Best-BlastP=>>nrprot 63% Identities = 174/360 (48%), Positives = 236/360 (65%), Gaps = 1/360 (0%) ref|NP_819557.1| phosphoserine aminotransferase [Coxiella burnetii RSA 493] gb|AAO90071.1| phosphoserine aminotransferase [Coxiella burnetii RSA 493] Length = 360

24.1 Best-BlastP=>>nrprot 23% Identities = 65/242 (26%), Positives = 117/242 (48%), Gaps = 20/242 (8%) ref|ZP_00096911.1| COG1738: Uncharacterized conserved protein [Novosphingiobium aromaticivorans] Length = 243

240.1 Best-BlastP=> nrprot 57% Identities = 144/316 (45%), Positives = 194/316 (61%), Gaps = 1/316 (0%) ref|NP_928703.1| Glucokinase (Glucose kinase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13698.1| Glucokinase (Glucose kinase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 321

2400.2 Best-BlastP=> nrprot 76% Identities = 181/285 (63%), Positives = 226/285 (79%), Gaps = 4/285 (1%) ref|NP_248803.1| probable cytochrome c oxidase assembly factor [Pseudomonas aeruginosa PA01] ref|ZP_00140528.1| COG0109: Polyphenyltransferase (cytochrome oxidase assembly factor) [Pseudomonas aeruginosa UCBPP-PA14] pir|F83632 probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAQ03503.1|AE004449_12 probable cytochrome c oxidase assembly factor [Pseudomonas aeruginosa PA01] Length = 304

2401.2 Best-BlastP=> nrprot 44% Identities = 57/167 (34%), Positives = 96/167 (57%), Gaps = 5/167 (2%) ref|ZP_00065551.1| COG1999: Uncharacterized protein SCO1/SenC/PrnC, involved in biogenesis of respiratory and photosynthetic systems [Microbulbifer degradans 2-40] Length = 219

2402.3 Best-BlastP=> nrprot 81% Identities = 316/450 (70%), Positives = 370/450 (82%), Gaps = 5/450 (1%) ref|NP_819057.1| chromosomal replication initiator protein DnaA [Coxiella burnetii] RSA 493] gb|AAO89571.1| chromosomal replication initiator protein DnaA [Coxiella burnetii] RSA 493] Length = 451

2402.3 Best-BlastP=> nrprot 67% Identities = 145/366 (39%), Positives = 247/366 (67%), Gaps = 2/366 (0%) ref|NP_796391.1| DNA polymerase III, beta chain [Vibrio parahaemolyticus RIMD 2210633] dbl|BAC58275.1| DNA polymerase III, beta chain [Vibrio parahaemolyticus] Length = 366

2404.2 Best-BlastP=> nrprot 67% Identities = 133/360 (36%), Positives = 205/360 (56%), Gaps = 12/360 (3%) ref|NP_759959.1| Recombinational DNA repair ATPase [Vibrio vulnificus CMCP6] spi|Q8DDJ1|RECF_VIBVU DNA replication and repair protein recF gb|AAO09486.1|AE016800_91 Recombinational DNA repair ATPase [Vibrio vulnificus CMCP6] Length = 359

2407.3 Best-BlastP=> nrprot 67% Identities = 370/794 (46%), Positives = 536/794 (67%), Gaps = 5/794 (0%) ref|NP_820311.1| phenylalanyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] gb|AAO90825.1| phenylalanyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] Length = 792

2409.3 Best-BlastP=> nrprot 100% Identities = 233/234 (99%), Positives = 234/234 (100%) emb|CAD42890.1| macrophage infectivity potentiator [Legionella pneumophila serogroup 8] Length = 236

241.2 Best-BlastP=> nrprot 76% Identities = 386/608 (63%), Positives = 470/608 (77%) ref|NP_718074.1| 6-phosphogluconate dehydratase [Shewanella oneidensis MR-1] Length = 608

2410.2 Best-BlastP=> nrprot 56% Identities = 157/390 (40%), Positives = 240/390 (61%), Gaps = 7/390 (1%) ref|NP_668353.1| ampg protein [Yersinia pestis KIM] Length = 510

2412.2 Best-BlastP=> nrprot 62% Identities = 245/553 (44%), Positives = 350/553 (63%), Gaps = 5/553 (0%) ref|NP_719011.1| DNA repair protein RecN [Shewanella oneidensis MR-1] gb|AAN56455.1|AE015782_7 DNA repair protein RecN [Shewanella oneidensis MR-1] Length = 552

2413.1 Best-BlastP=> nrprot 73% Identities = 46/67 (68%), Positives = 51/67 (76%), Gaps = 1/67 (1%) ref|ZP_00065318.1| COG1278: Cold shock proteins [Microbulbifer degradans 2-40] Length = 69

2414.2 Best-BlastP=> >nrprot 46% Identities = 86/333 (25%), Positives = 166/333 (49%), Gaps = 15/333 (4%) ref|NP_819780.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] gb|AAO90294.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] Length = 348

2415.2 Best-BlastP=> >nrprot 37% Identities = 69/273 (25%), Positives = 121/273 (44%), Gaps = 25/273 (9%) ref|ZP_00087134.1| COG2162: Arylamine N-acetyltransferase [Pseudomonas fluorescens PfO-1] Length = 292

2418.2 Best-BlastP=> >nrprot 63% Identities = 106/234 (45%), Positives = 154/234 (65%) ref|NP_821026.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO91540.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 237

2419.3 Best-BlastP=> >nrprot 48% Identities = 74/222 (33%), Positives = 110/222 (49%), Gaps = 10/222 (4%) ref|NP_626575.1| putative dipeptidase [Streptomyces coelicolor A3(2)] emb|CAB93448.1| putative dipeptidase [Streptomyces coelicolor A3(2)] Length = 218

2421.2 Best-BlastP=> >nrprot 68% Identities = 266/502 (52%), Positives = 345/502 (68%), Gaps = 12/502 (2%) ref|NP_639214.1| competence related protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM43105.1| competence related protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 506

2422.3 Best-BlastP=> >nrprot 49% Identities = 31/123 (25%), Positives = 64/123 (52%), Gaps = 3/123 (2%) ref|NP_703938.1| 6-pyruvoyl tetrahydropterin synthase, putative [Plasmodium falciparum 3D7] emb|CAD50550.1| 6-pyruvoyl tetrahydropterin synthase, putative [Plasmodium falciparum 3D7] Length = 173

2423.2 Best-BlastP=> >nrprot 63% Identities = 163/360 (45%), Positives = 237/360 (65%), Gaps = 3/360 (0%) ref|NP_820807.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91321.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 388

2424.3 Best-BlastP=> >nrprot 63% Identities = 92/176 (52%), Positives = 120/176 (68%), Gaps = 1/176 (0%) ref|NP_407270.1| putative membrane protein [Yersinia pestis] pir|AF0465 probable membrane protein YPO3822 [imported] - Yersinia pestis (strain CO92) emb|CAC93290.1| putative membrane protein [Yersinia pestis CO92] Length = 222

2425.2 Best-BlastP=> >nrprot 51% Identities = 72/187 (38%), Positives = 110/187 (58%), Gaps = 1/187 (0%) ref|NP_419508.1| conserved hypothetical protein [Caulobacter crescentus CB15] pir|H87334 conserved hypothetical protein CC0691 [imported] - Caulobacter crescentus gb|AAK22676.1| conserved hypothetical protein [Caulobacter crescentus CB15] Length = 208

2426.2 Best-BlastP=> >nrprot No Hits found

2427.4 Best-BlastP=> >nrprot 61% Identities = 37/65 (56%), Positives = 44/65 (67%) ref|ZP_00091135.1| COG2852: Uncharacterized protein conserved in bacteria [Azotobacter vinelandii] Length = 150

2428.2 Best-BlastP=> >nrprot 58% Identities = 36/85 (42%), Positives = 55/85 (64%), Gaps = 7/85 (8%) ref|NP_681031.1| ORF_ID:t|0240~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP_681232.1| ORF_ID:t|0442~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP_681541.1| ORF_ID:t|0752~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP_681563.1| ORF_ID:t|0774~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP_681789.1| ORF_ID:t|0999~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP_682035.1| ORF_ID:t|1245~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP_682721.1| ORF_ID:t|1931~putative transposase [Thermosynechococcus elongatus BP-1] dbj|BAC07793.1| ORF_ID:t|0240~putative transposase [Thermosynechococcus elongatus BP-1] dbj|BAC07994.1| ORF_ID:t|0442~putative transposase [Thermosynechococcus elongatus BP-1] dbj|BAC08303.1| ORF_ID:t|0752~p

2429.2 Best-BlastP=> >nrprot 69% Identities = 159/294 (54%), Positives = 211/294 (71%), Gaps = 1/294 (0%) ref|NP_792069.1| moxR protein, putative [Pseudomonas syringae pv. tomato str. DC3000] Length = 305

243.2 Best-BlastP=> >nrprot 67% Identities = 163/295 (55%), Positives = 210/295 (71%), Gaps = 1/295 (0%) dbj|BAC95199.1| putative adenine-specific methylase [Vibrio vulnificus YJ016] Length = 310

2430.2 Best-BlastP=> >nrprot 63% Identities = 172/365 (47%), Positives = 229/365 (62%), Gaps = 12/365 (3%) ref|NP_840708.1| Domain of unknown function DUF59 [Nitrosomonas europaea ATCC 19718] emb|CAD84535.1| Domain of unknown function DUF59 [Nitrosomonas europaea ATCC 19718] Length = 361

2432.2 Best-BlastP=> >nrprot 70% Identities = 233/378 (61%), Positives = 292/378 (77%) ref|NP_719320.1| ATP-dependent RNA helicase, DEAD box family [Shewanella oneidensis MR-1] dbj|AAN56764.1|AE015812_3 ATP-dependent RNA helicase, DEAD box family [Shewanella oneidensis MR-1] Length = 535

2434.2 Best-BlastP=> >nrprot 70% Identities = 184/388 (47%), Positives = 270/388 (69%), Gaps = 8/388 (2%) ref|NP_903067.1| probable stearoyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] dbj|AAQ61061.1| probable stearoyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] Length = 405

2436.2 Best-BlastP=> >nrprot No Hits found

2438.2 Best-BlastP=> >nrprot 79% Identities = 59/92 (64%), Positives = 75/92 (81%) dbj|AAL59720.1| unknown [Vibrio cholerae] Length = 92

2439.2 Best-BlastP=> >nrprot 86% Identities = 81/107 (75%), Positives = 93/107 (86%), Gaps = 1/107 (0%) dbj|AAL59719.1| unknown [Vibrio cholerae] Length = 107

244.1 Best-BlastP=> >nrprot 80% Identities = 230/350 (65%), Positives = 285/350 (81%) dbj|BAC95198.1| chorismate synthase [Vibrio vulnificus YJ016] Length = 377

2441.2 Best-BlastP=> >nrprot 51% Identities = 134/398 (33%), Positives = 209/398 (52%), Gaps = 16/398 (4%) ref|NP_779202.1| phage-related integrase [Xylella fastidiosa Temecula1] dbj|AAO28851.1| phage-related integrase [Xylella fastidiosa Temecula1] Length = 410

2442.2 Best-BlastP=> >nrprot 36% Identities = 93/315 (29%), Positives = 158/315 (50%), Gaps = 2/315 (6%) ref|NP_435846.1| Probable adenylylate cyclase [Sinorhizobium meliloti] pir|IH95336 probable adenylylate cyclase (EC 4.6.1.1) [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA dbj|AAK65258.1| Probable adenylylate cyclase [Sinorhizobium meliloti] Length = 584

2443.2 Best-BlastP=> >nrprot 36% Identities = 55/232 (23%), Positives = 100/232 (43%), Gaps = 10/232 (4%) ref|ZP_00068000.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 260

2445.4 Best-BlastP=> >nrprot 79% Identities = 635/925 (68%), Positives = 746/925 (80%), Gaps = 6/925 (0%) ref|NP_820536.1| ribonucleoside-diphosphate reductase, alpha subunit [Coxiella burnetii RSA 493] dbj|AO91050.1| ribonucleoside-diphosphate reductase, alpha subunit [Coxiella burnetii RSA 493] Length = 941

2447.3 Best-BlastP=> >nrprot 19% Identities = 35/121 (28%), Positives = 62/121 (51%), Gaps = 6/121 (4%) ref|NP_599246.1| protein associating with small stress protein PASS1 [Rattus norvegicus] dbj|AAD48846.1|AF168362_1 protein associating with small stress protein PASS1 [Rattus norvegicus] Length = 428

2448.3 Best-BlastP=>>nprot 54% Identities = 94/226 (41%), Positives = 142/226 (62%), Gaps = 8/226 (3%) refNP_821052.1] conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91566.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 268

2451 Best-BlastP=>>nprot 97% Identities = 331/340 (97%), Positives = 332/340 (97%) sp|O31219|DHAS_LEGPN Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) gb|AAC46292.1| aspartate-B-semialdehyde dehydrogenase [Legionella pneumophila] Length = 347

2450.3 Best-BlastP=>>nprot 67% Identities = 299/616 (48%), Positives = 24/616 (3%) refNP_842471.1] ATPase component ABC-type dipeptide/oligopeptide/nickel transport system [Nitrosomonas europaea ATCC 19718] emb|CAD86392.1| ATPase component ABC-type dipeptide/oligopeptide/nickel transport system [Nitrosomonas europaea ATCC 19718] Length = 693

2453.4 Best-BlastP=>>nprot 75% Identities = 554/897 (61%), Positives = 689/897 (76%), Gaps = 3/897 (0%) ref|ZP_00096570.1| COG0474: Cation transport ATPase [Novosphingobium aromaticivorans] Length = 911

2456.2 Best-BlastP=>>nprot 78% Identities = 201/314 (64%), Positives = 251/314 (79%) refNP_820493.1] acetyl-CoA carboxylase, carboxytransferase, alpha subunit [Coxiella burnetii RSA 493] gb|AAO91007.1| acetyl-CoA carboxylase, carboxytransferase, alpha subunit [Coxiella burnetii RSA 493] Length = 316

2457.2 Best-BlastP=>>nprot 46% Identities = 75/215 (34%), Positives = 114/215 (53%), Gaps = 16/215 (7%) ref|ZP_00107102.1| COG2091: Phosphopantetheinyl transferase [Nostoc punctiforme] Length = 239

2458.2 Best-BlastP=>>nprot 68% Identities = 190/371 (51%), Positives = 259/371 (69%) refNP_819627.1] oxygen-independent coproporphyrinogen III oxidase, putative [Coxiella burnetii RSA 493] gb|AAO90141.1| oxygen-independent coproporphyrinogen III oxidase, putative [Coxiella burnetii RSA 493] Length = 375

2459.1 Best-BlastP=>>nprot 69% Identities = 94/176 (53%), Positives = 131/176 (74%), Gaps = 1/176 (0%) refNP_715832.1] MutT/nudix family protein [Shewanella oneidensis MR-1] gb|AAN53277.1|AE015469_1 MutT/nudix family protein [Shewanella oneidensis MR-1] Length = 183

2460.3 Best-BlastP=>>nprot 62% Identities = 230/569 (40%), Positives = 358/569 (62%), Gaps = 12/569 (2%) refNP_820129.1] oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] gb|AAO90643.1| oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] Length = 669

2461.2 Best-BlastP=>>nprot 57% Identities = 33/49 (67%), Positives = 4/49 (83%) refNP_051689.1] Integrase/recombinase XerD, putative [Deinococcus radiodurans] pir|G75636 probable integrase/recombinase XerD - Deinococcus radiodurans (strain R1) gb|AAT12667.1|AE001827_5 integrase/recombinase XerD, putative [Deinococcus radiodurans] Length = 236

2462.2 Best-BlastP=>>nprot 33% Identities = 20/38 (52%), Positives = 25/38 (65%) ref|ZP_00111545.1| COG4644: Transposase and inactivated derivatives, TnpA family [Nostoc punctiforme] Length = 1014

2464.2 Best-BlastP=>>nprot 67% Identities = 61/108 (56%), Positives = 80/108 (74%) refNP_841625.1] transposase [Nitrosomonas europaea ATCC 19718] ref|NP_842205.1| transposase [Nitrosomonas europaea ATCC 19718] refNP_842439.1| transposase [Nitrosomonas europaea ATCC 19718] emb|CAD85497.1| transposase [Nitrosomonas europaea ATCC 19718] emb|CAD86112.1| transposase [Nitrosomonas europaea ATCC 19718] emb|CAD86359.1| transposase [Nitrosomonas europaea ATCC 19718] Length = 122

2466.3 Best-BlastP=>>nrprot 52%
[Coxiella burnetii RSA 493] gb|AAO89894.1| aminopeptidase N
Identities = 316/879 (35%), Positives = 473/879 (53%), Gaps = 49/879 (5%) ref|NP_819380.1| aminopeptidase N
Length = 878

2468.2 Best-BlastP=>>nrprot 39%
[Methanoscarcina mazei Goe1] gb|AAM322449.1| putative hydrolase
Identities = 76/253 (30%), Positives = 122/253 (48%), Gaps = 18/253 (7%) ref|NP_634577.1| putative hydrolase
Length = 279

2469.2 Best-BlastP=>>nrprot 44%
protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60541.1| conserved hypothetical protein [Vibrio parahaemolyticus]
Identities = 138/423 (32%), Positives = 216/423 (51%), Gaps = 7/423 (1%) ref|NP_798657.1| conserved hypothetical
Length = 483

247.1 Best-BlastP=>>nrprot 29%
conserved in bacteria
[Microbulbifer degradans 2-40] Length = 190

2471.3 Best-BlastP=>>nrprot 55%
protein RibD [Coxiella burnetii RSA 493] gb|AAO90187.1| riboflavin biosynthesis
Identities = 129/344 (37%), Positives = 199/344 (57%), Gaps = 6/344 (1%) ref|NP_819673.1| riboflavin biosynthesis
Length = 354

2472.2 Best-BlastP=>>nrprot 61%
[Coxiella burnetii RSA 493] gb|AAO90524.1| dethiobiotin synthetase [Coxiella burnetii RSA 493]
Identities = 87/219 (39%), Positives = 131/219 (59%), Gaps = 12/219 (5%) ref|NP_820010.1| dethiobiotin synthetase
Length = 242

2473.1 Best-BlastP=>>nrprot 54%
protein [Coxiella burnetii RSA 493] gb|AAO91055.1| conserved hypothetical protein [Coxiella burnetii RSA 493]
Identities = 35/70 (50%), Positives = 48/70 (68%), Gaps = 3/70 (4%) ref|NP_820541.1| conserved hypothetical
Length = 91

2474.1 Best-BlastP=>>nrprot 72%
protein [Coxiella burnetii RSA 493] gb|AAO91056.1| conserved hypothetical protein [Coxiella burnetii RSA 493]
Identities = 105/192 (54%), Positives = 152/192 (79%), Gaps = 2/192 (1%) ref|NP_820542.1| conserved hypothetical
Length = 209

2477.1 Best-BlastP=>>nrprot 52%
protein [Coxiella burnetii RSA 493] gb|AAO90508.1| rare lipoprotein A family
Identities = 68/115 (59%), Positives = 85/115 (73%), Gaps = 2/115 (1%) ref|NP_819994.1| rare lipoprotein A family
Length = 261

2479.2 Best-BlastP=>>nrprot No Hits found

248.2 Best-BlastP=>>nrprot 59%
protein [Coxiella burnetii RSA 493] gb|AAO90798.1| ankyrin repeat domain
Identities = 191/456 (41%), Positives = 278/456 (60%), Gaps = 7/456 (1%) ref|NP_820284.1| ankyrin repeat domain
Length = 465

2481.4 Best-BlastP=>>nrprot 77%
phosphonomutase 2 [Escherichia coli O157:H7 EDL933] ref|NP_308412.1| putative phosphonomutase 2 [Escherichia coli O157:H7] pir|A90677
probable phosphonomutase 2 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|ID85527 probable
phosphonomutase 2 [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gb|AAG54680.1|AE005212_5 putative
phosphonomutase 2 [Escherichia coli O157:H7 EDL933] dbj|BAB33808.1| putative phosphonomutase 2 [Escherichia coli O157:H7]
Length = 296

2482.1 Best-BlastP=>>nrprot 59%
RSA 493] gb|AAO91503.1| conserved domain protein [Coxiella burnetii RSA 493]
Identities = 75/125 (60%), Positives = 101/125 (80%) ref|NP_820989.1| conserved domain protein [Coxiella burnetii
Length = 127

2483.2 Best-BlastP=>>nrprot No Hits found

2485.3 Best-BlastP=> >nrprot No Hits found

2486.3 Best-BlastP=> >nrprot 55% Identities = 188/514 (36%), Positives = 280/514 (54%), Gaps = 43/514 (8%) ref|ZP_00087809.1| COG2202: FOG: PAS/PAC domain [Pseudomonas fluorescens PfO-1] Length = 757

2488.2 Best-BlastP=> >nrprot No Hits found

2489.2 Best-BlastP=> >nrprot No Hits found

249.4 Best-BlastP=> >nrprot 97% Identities = 558/575 (97%), Positives = 562/575 (97%), Gaps = 1/575 (0%) gb|AAC12716.1| pilus assembly protein PilB [Legionella pneumophila] Length = 575

2490.2 Best-BlastP=> >nrprot No Hits found

2492.2 Best-BlastP=> >nrprot No Hits found

2493.2 Best-BlastP=> >nrprot 67% Identities = 99/203 (48%), Positives = 135/203 (66%), Gaps = 10/203 (4%) ref|NP_929371.1| Holliday junction DNA helicase [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE14404.1| Holliday junction DNA helicase [Photobacterium laumondii TTO1] Length = 205

2495.2 Best-BlastP=> >nrprot 69% Identities = 93/170 (54%), Positives = 121/170 (71%), Gaps = 1/170 (0%) ref|NP_231481.1| crossover junction endodeoxyribonuclease RuvC [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KR00|RUVCF_VIBCH Crossover junction endodeoxyribonuclease RuvC (Holliday junction resolvase ruvC) pir|H82149 crossover junction endodeoxyribonuclease RuvC VC1847 [imported] - endodeoxyribonuclease RuvC [Vibrio cholerae O1 biovar eltor str. N16961] Length = 173

25.1 Best-BlastP=> >nrprot 46% Identities = 46/124 (37%), Positives = 72/124 (58%), Gaps = 3/124 (2%) ref|NP_488674.1| probable cytosine deaminase [Nostoc sp. PCC 7120] pir|AB2385 hypothetical protein alr4634 [imported] - Nostoc sp. (strain PCC 7120) db|BAB76333.1| ORF_ID:alr4634~probable cytosine deaminase [Nostoc sp. PCC 7120] Length = 140

250.1 Best-BlastP=> >nrprot 98% Identities = 398/406 (98%), Positives = 400/406 (98%) gb|AAC12717.1| pilus assembly protein PilC [Legionella pneumophila] Length = 406

2501.2 Best-BlastP=> >nrprot 70% Identities = 213/412 (51%), Positives = 294/412 (71%), Gaps = 12/412 (2%) ref|NP_819142.1| tolB protein [Coxiella burnetii RSA 493] sp|Q83F59|TOLB_COXBU TolB protein precursor gb|AAO89656.1| tolB protein [Coxiella burnetii RSA 493] Length = 437

2504.4 Best-BlastP=> >nrprot 51% Identities = 106/301 (35%), Positives = 164/301 (54%), Gaps = 34/301 (11%) ref|NP_718333.1| tolA protein [Shewanella oneidensis MR-1] gb|AAN55777.1|AE015714_4 tolA protein [Shewanella oneidensis MR-1] Length = 345

2506.2 Best-BlastP=> >nrprot 83% Identities = 238/338 (70%), Positives = 282/338 (83%) gb|AAN87043.1| HypE [Thiocapsa roseopersicina] Length = 360

2508.3 Best-BlastP=> >nrprot 77% Identities = 234/375 (62%), Positives = 285/375 (76%), Gaps = 6/375 (1%) ref|ZP_00021585.1| COG0409: Hydrogenase maturation factor [Ralstonia metallidurans] Length = 380

2509.3 Best-BlastP=> >nrprot No Hits found

251.2 Best-BlastP=> >nrprot 97% Identities = 277/287 (96%), Positives = 281/287 (97%) sp|O68433|LEP4_LEGPN Type 4 prephilin-like proteins leader peptide processing enzyme [Includes: Leader peptidase (Prephilin peptidase); N-methyltransferase] gb|AAC12718.1| type IV prephilin-like protein specific leader peptidase PilD [Legionella pneumophila] Length = 287

2510.2 Best-BlastP=> >nrprot 69% Identities = 310/637 (48%), Positives = 427/637 (67%), Gaps = 19/637 (2%) ref|ZP_00067611.1| COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Microbulbifer degradans 2-40] Length = 637

2514.3 Best-BlastP=> >nrprot 74% Identities = 52/84 (61%), Positives = 67/84 (79%), Gaps = 2/84 (2%) ref|ZP_00128272.1| COG0851: Septum formation topological specificity factor [Pseudomonas syringae pv. syringae B728a] Length = 84

2517.2 Best-BlastP=> >nrprot 65% Identities = 197/336 (58%), Positives = 240/336 (71%), Gaps = 2/336 (0%) ref|NP_634897.1| L-sorbose dehydrogenase [Methanosarcina mazei Goe1] gb|AAM32569.1| L-sorbose dehydrogenase [Methanosarcina mazei Goe1] Length = 381

2518.4 Best-BlastP=> >nrprot 86% Identities = 123/179 (68%), Positives = 156/179 (87%) ref|NP_250365.1| GTP cyclohydrolase I precursor [Pseudomonas aeruginosa PA01] sp|Q9i351|GC12_PSEAE GTP cyclohydrolase I 2 (GTP-CH-I-2) pir|C83435 GTP cyclohydrolase I precursor PA1674 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05063.1|AE004595_2 GTP cyclohydrolase I precursor [Pseudomonas aeruginosa PAO1] Length = 181

252.2 Best-BlastP=> >nrprot 40% Identities = 86/303 (28%), Positives = 161/303 (53%), Gaps = 13/303 (4%) ref|NP_819235.1| CAA_X amino terminal protease family protein [Coxiella burnetii RSA 493] gb|AAO89749.1| CAA_X amino terminal protease family protein [Coxiella burnetii RSA 493] Length = 297

2520.4 Best-BlastP=> >nrprot 73% Identities = 64/111 (57%), Positives = 84/111 (75%), Gaps = 1/111 (0%) ref|NP_819816.1| H1T family protein [Coxiella burnetii RSA 493] gb|AAO90330.1| H1T family protein [Coxiella burnetii RSA 493] Length = 113

2521.4 Best-BlastP=> >nrprot 71% Identities = 205/348 (58%), Positives = 251/348 (72%), Gaps = 1/348 (0%) ref|ZP_00028857.1| COG1064: Zn-dependent alcohol dehydrogenases [Burkholderia fungorum] Length = 377

2522.1 Best-BlastP=> >nrprot No Hits found

2523.1 Best-BlastP=> >nrprot 54% Identities = 46/128 (35%), Positives = 73/128 (57%) ref|ZP_00011417.1| hypothetical protein [Rhodopseudomonas palustris] Length = 135

2524.2 Best-BlastP=> >nrprot 51% Identities = 71/192 (36%), Positives = 105/192 (54%), Gaps = 7/192 (3%) sp|Q92J7|DEF2_RICCN Peptide deformylase 2 (PDF 2) (Polypeptide deformylase 2) Length = 202

2526.3 Best-BlastP=> >nrprot 13% Identities = 40/132 (30%), Positives = 59/132 (44%), Gaps = 16/132 (12%) ref|NP_440029.1| acetylpolyamine aminohydrolase [Synechocystis sp. PCC 6803] sp|P72702|Y245_SYNY3 Hypothetical protein sli0245 pir|S74557 acetylpolyamine aminohydrolase - Synechocystis sp. (strain PCC 6803) dbj|BAA16709.1| acetylpolyamine aminohydrolase [Synechocystis sp. PCC 6803] Length = 304

2528.3 Best-BlastP=> >nrprot 41% Identities = 53/236 (22%), Positives = 105/236 (44%), Gaps = 7/236 (2%) ref|NP_845027.1| acetyltransferase, GNAT family [Bacillus anthracis str. Ames] gb|AAP2651.3.1| acetyltransferase, GNAT family [Bacillus anthracis str. Ames] Length = 266

2530.3 Best-BlastP=> >nrprot 63% Identities = 266/626 (42%), Positives = 401/626 (64%), Gaps = 8/626 (1%) ref|NP_900243.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58249.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] Length = 621

2533.3 Best-BlastP=>>nrprot 52% Identities = 88/286 (30%), Positives = 158/286 (55%), Gaps = 4/286 (1%) ref|NP_763522.1| Transcriptional regulator [Vibrio vulnificus CMCP6] gb|AAO08512.1|AE016813_264 Transcriptional regulator [Vibrio vulnificus CMCP6] Length = 307

2535.2 Best-BlastP=>>nrprot 70% Identities = 200/351 (56%), Positives = 253/351 (72%) ref|NP_519918.1| PROBABLE PYRUVATE DEHYDROGENASE E1 COMPONENT (ALPHA SUBUNIT) OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum] emb|CAD15499.1| PROBABLE PYRUVATE DEHYDROGENASE E1 COMPONENT (ALPHA SUBUNIT) OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum] Length = 363

2536.2 Best-BlastP=>>nrprot 57% Identities = 255/451 (56%), Gaps = 36/451 (7%) ref|NP_798254.1| para-aminobenzoate synthase, component I [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60138.1| para-aminobenzoate synthase, component I [Vibrio parahaemolyticus] Length = 454

2538.2 Best-BlastP=>>nrprot 78% Identities = 245/394 (62%), Positives = 309/394 (78%) ref|NP_901758.1| acetyl-CoA C-acetyltransferase [Chromobacterium violaceum ATCC 12472] gb|AAQ59760.1| acetyl-CoA C-acetyltransferase [Chromobacterium violaceum ATCC 12472] Length = 394

254.2 Best-BlastP=>>nrprot 49% Identities = 275/851 (32%), Positives = 428/851 (50%), Gaps = 29/851 (3%) ref|NP_490573.1| ATP-binding protein [Salmonella typhimurium LT2] gb|AAL23492.1| conjugative transfer: assembly [Salmonella typhimurium LT2] Length = 882

2542.2 Best-BlastP=>>nrprot 61% Identities = 214/405 (52%), Positives = 282/405 (69%), Gaps = 8/405 (1%) ref|ZP_00014043.1| COG0260: Leucyl aminopeptidase [Rhodospirillum rubrum] Length = 444

2544.3 Best-BlastP=>>nrprot 5% Identities = 36/130 (27%), Positives = 68/130 (52%), Gaps = 7/130 (5%) ref|NP_711281.1| outer membrane efflux protein [Leptospira interrogans serovar lai str. 56601] gb|AAN48299.1|AE011292_12 outer membrane efflux protein [Leptospira interrogans serovar lai str. 56601] Length = 533

2545.2 Best-BlastP=>>nrprot No Hits found

2546.4 Best-BlastP=>>nrprot 47% Identities = 155/432 (35%), Positives = 239/432 (55%), Gaps = 21/432 (4%) emb|CAE02834.1| OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)] Length = 487

2549.3 Best-BlastP=>>nrprot No Hits found

255.1 Best-BlastP=>>nrprot 39% Identities = 23/83 (27%), Positives = 44/83 (53%), Gaps = 1/83 (1%) ref|NP_762592.1| Unknown [Vibrio vulnificus CMCP6] gb|AAO07582.1|AE016810_85 Unknown [Vibrio vulnificus CMCP6] Length = 114

2550.2 Best-BlastP=>>nrprot 99% Identities = 443/449 (98%), Positives = 446/449 (99%) gb|AAB52239.1| nucleotide binding protein Fli [Legionella pneumophila] Length = 449

2551.2 Best-BlastP=>>nrprot 34% Identities = 74/75 (98%), Positives = 74/75 (98%) gb|AAB52238.1| FliH [Legionella pneumophila] Length = 75

2553.3 Best-BlastP=>>nrprot 76% Identities = 168/326 (51%), Positives = 251/326 (76%) ref|NP_791782.1| flagellar motor switch protein FliG [Pseudomonas syringae pv. tomato str. DC3000] dbj|DC3000.1| flagellar motor switch protein FliG [Pseudomonas syringae pv. tomato str. DC3000] Length = 333

2555.5 Best-BlastP=>>nrprot No Hits found

2557.4 Best-BlastP=>>nrprot 61% Identities = 70/135 (51%), Positives = 91/135 (67%) ref|ZP_00085924.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 141

2559.3 Best-BlastP=>>nrprot 85% Identities = 243/333 (72%), Positives = 289/333 (86%) ref|NP_438478.1| Holliday junction DNA helicase [Haemophilus influenzae Rd] sp|P44631|RUVB_HAEIN Holliday junction DNA helicase rvB pir|BB64061 DNA-binding protein rvB - Haemophilus influenzae (strain Rd KW20) gb|AAC21975.1| Holliday junction DNA helicase (rvB) [Haemophilus influenzae Rd] Length = 335

2561.1 Best-BlastP=>>nrprot 52% Identities = 79/194 (40%), Positives = 109/194 (56%), Gaps = 14/194 (7%) ref|NP_762593.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO07583.1|AE016810_86 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 226

2560.3 Best-BlastP=>>nrprot 98% Identities = 186/187 (99%), Positives = 186/187 (99%) gb|AAQ18125.1| RpoE [Legionella pneumophila] Length = 187

2562.2 Best-BlastP=>>nrprot No Hits found

2565.4 Best-BlastP=>>nrprot 55% Identities = 88/226 (38%), Positives = 129/226 (57%), Gaps = 17/226 (7%) ref|NP_651138.1| CG6763-PA [Drosophila melanogaster] gb|AAF56122.1| CG6763-PA [Drosophila melanogaster] gb|AAL68281.1| RE28575p [Drosophila melanogaster] Length = 354

2567.2 Best-BlastP=>>nrprot 42% Identities = 53/201 (26%), Positives = 92/201 (45%), Gaps = 3/201 (1%) ref|NP_683243.1| ORF_ID:t|2454~unknown protein [Thermosynechococcus elongatus BP-1] dbj|BAC10005.1| ORF_ID:t|2454~unknown protein [Thermosynechococcus elongatus BP-1] Length = 253

2568.1 Best-BlastP=>>nrprot No Hits found

2569.3 Best-BlastP=>>nrprot 56% Identities = 80/207 (38%), Positives = 122/207 (58%), Gaps = 18/207 (8%) ref|NP_840655.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD84482.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 253

2570.2 Best-BlastP=>>nrprot 64% Identities = 144/374 (38%), Positives = 243/374 (64%), Gaps = 4/374 (1%) ref|NP_518286.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD13693.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 381

2571.2 Best-BlastP=>>nrprot 64% Identities = 135/292 (46%), Positives = 199/292 (68%), Gaps = 3/292 (1%) ref|ZP_00056519.1| COG1131: ABC-type multidrug transport system, ATPase component [Magnetospirillum magnetotacticum] Length = 308

2573.3 Best-BlastP=>>nrprot 98% Identities = 188/192 (97%), Positives = 190/192 (98%) gb|AAK00281.1|AF288536_3 unknown [Legionella longbeachae] Length = 192

2576.2 Best-BlastP=>>nrprot 99% Identities = 319/319 (100%), Positives = 319/319 (100%) gb|AAM00641.1| putative Na/Ca antiporter [Legionella pneumophila] Length = 319

2578.2 Best-BlastP=>>nrprot 99% Identities = 234/234 (100%), Positives = 234/234 (100%) gb|AAM00640.1| unknown [Legionella pneumophila] Length = 234

2579.2 Best-BlastP=>>nrprot 62% Identities = 54/135 (40%), Positives = 89/135 (65%) ref|NP_903458.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61450.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 159

258.2 Best-BlastP=>>nrprot 56% Identities = 161/309 (52%), Positives = 213/309 (68%), Gaps = 4/309 (1%) gb|AAM90716.1| TraU [Salmonella typhi] Length = 331

2580.2 Best-BlastP=> >nrprot 78% Identities = 155/249 (62%), Positives = 198/249 (79%) ref|ZP_00133889.1| COG2226: Methylase involved in ubiquinone/maequinone biosynthesis [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 258

2582.3 Best-BlastP=> >nrprot 47% Identities = 242/883 (27%), Positives = 412/883 (46%), Gaps = 56/883 (6%) ref|NP_842182.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD86089.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 909

2583.3 Best-BlastP=> >nrprot 38% Identities = 40/156 (25%), Positives = 72/156 (46%), Gaps = 23/156 (14%) ref|NP_764254.1| Na+/H+ antiporter-like protein [Staphylococcus epidermidis ATCC 12228] gb|AAO04296.1|AE016746_86 Na+/H+ antiporter-like protein [Staphylococcus epidermidis ATCC 12228] Length = 614

2585.2 Best-BlastP=> >nrprot 13% Identities = 45/193 (23%), Positives = 77/193 (39%), Gaps = 30/193 (15%) ref|NP_866179.1| hypothetical protein-transmembrane region and signal peptide prediction [Pirellula sp.] emb|CAD73865.1| hypothetical protein-transmembrane region and signal peptide prediction [Pirellula sp.] Length = 500

2587.2 Best-BlastP=> >nrprot 59% Identities = 114/283 (40%), Positives = 169/283 (59%), Gaps = 4/283 (1%) ref|ZP_00094776.1| COG0583: Transcriptional regulator [Novosphingobium aromaticivorans] Length = 290

2590.3 Best-BlastP=> >nrprot 60% Identities = 125/288 (43%), Positives = 184/288 (63%), Gaps = 3/288 (1%) ref|ZP_00096382.1| COG0121: Predicted glutamine amidotransferase [Novosphingobium aromaticivorans] Length = 444

2591.3 Best-BlastP=> >nrprot 66% Identities = 182/348 (52%), Positives = 234/348 (67%), Gaps = 2/348 (0%) ref|NP_2333382.1| NADH-dependent flavin oxidoreductase, Oye family VCA0998 [imported] - Vibrio cholerae O1 biovar eltor str. N16961 pir|H82391 NADH-dependent flavin oxidoreductase, Oye family [Vibrio cholerae O1 biovar eltor str. N16961] gb|AAF96894.1| NADH-dependent flavin oxidoreductase, Oye family [Vibrio cholerae O1 biovar eltor str. N16961] Length = 347

2592.4 Best-BlastP=> >nrprot No Hits found

2593.3 Best-BlastP=> >nrprot 62% Identities = 98/248 (39%), Positives = 161/248 (64%), Gaps = 7/248 (2%) ref|NP_250139.1| flagellar biosynthetic protein FlIR [Pseudomonas aeruginosa PA01] pir|B83465 flagellar biosynthetic protein FlIR PA1448 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04837.1|AE04574_8 flagellar biosynthetic protein FlIR [Pseudomonas aeruginosa PAO1] Length = 258

2595.4 Best-BlastP=> >nrprot 77% Identities = 142/241 (58%), Positives = 193/241 (80%), Gaps = 1/241 (0%) ref|NP_746469.1| flagellar biosynthetic protein FlIP [Pseudomonas putida KT2440] gb|AAD01927.2|FlIP [Pseudomonas putida] gb|AAN69933.1|AE016632_4 flagellar biosynthetic protein FlIP [Pseudomonas putida KT2440] Length = 251

2597.4 Best-BlastP=> >nrprot 99% Identities = 225/226 (99%), Positives = 226/226 (100%) gb|AAM00392.1|AF386079_2 CcmB [Legionella pneumophila] Length = 226

2598.3 Best-BlastP=> >nrprot 59% Identities = 76/216 (35%), Positives = 130/216 (60%), Gaps = 6/216 (2%) ref|NP_799389.1| conserved hypothetical protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61273.1| conserved hypothetical protein [Vibrio parahaemolyticus] Length = 219

2599.4 Best-BlastP=> >nrprot 82% Identities = 380/556 (68%), Positives = 461/556 (82%), Gaps = 2/556 (0%) ref|NP_927905.1| ATP-binding protein YjjK [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE12850.1| ATP-binding protein YjjK [Photorhabdus luminescens subsp. laumondii TTO1] Length = 555

26.1 Best-BlastP=> >nrprot 30% Identities = 57/132 (43%), Positives = 8/1132 (61%), Gaps = 6/132 (4%) ref|ZP_00031525.1| hypothetical protein [Burkholderia fungorum] Length = 153

2600.4 Best-BlastP=> >nrprot 84% Identities = 239/341 (70%), Positives = 287/341 (84%) ref|NP_931999.1| threonine 3-dehydrogenase [Photorhabdus luminescens subsp. laumontii TTO1] Length = 341

2602.2 Best-BlastP=> >nrprot 63% Identities = 144/273 (52%), Positives = 188/273 (68%), Gaps = 2/273 (0%) ref|ZP_00067856.1| COG0061: Predicted sugar kinase [Microbulbifer degradans 2-40] Length = 294

2604.3 Best-BlastP=> >nrprot 83% Identities = 437/603 (72%), Positives = 511/603 (84%) ref|ZP_00043195.1| COG1217: Predicted membrane GTPase involved in stress response [Magnetococcus sp. MC-1] Length = 611

2605.3 Best-BlastP=> >nrprot 53% Identities = 300/814 (36%), Positives = 445/814 (54%), Gaps = 23/814 (2%) ref|NP_111982.1| Type III restriction-modification enzyme, helicase subunit [Thermoplasma volcanium] dbj|BAB60631.1| TVG1539639 [Thermoplasma volcanium] Length = 843

2607.2 Best-BlastP=> >nrprot 34% Identities = 87/295 (29%), Positives = 141/295 (47%), Gaps = 10/295 (3%) ref|NP_8277021.1| hypothetical protein [Streptomyces avermitilis MA-4680] dbj|BAC73556.1| hypothetical protein [Streptomyces avermitilis MA-4680] Length = 416

2609.2 Best-BlastP=> >nrprot No Hits found

2611.1 Best-BlastP=> >nrprot No Hits found

2616.1 Best-BlastP=> >nrprot 35% Identities = 58/180 (32%), Positives = 106/180 (58%), Gaps = 1/180 (0%) ref|NP_624053.1| predicted transposase [Thermoanaerobacter tengcongensis] gb|AAC25657.1| predicted transposase [Thermoanaerobacter tengcongensis] Length = 267

2619.1 Best-BlastP=> >nrprot 40% Identities = 37/137 (27%), Positives = 62/137 (45%), Gaps = 39/137 (28%) emb|CAB46580.1| IS1400 transposase B [Yersinia enterocolitica] Length = 294

262.3 Best-BlastP=> >nrprot 41% Identities = 123/341 (36%), Positives = 184/341 (53%), Gaps = 21/341 (6%) ref|NP_827717.1| putative quinolinate synthetase [Streptomyces avermitilis MA-4680] dbj|BAC73752.1| putative quinolinate synthetase [Streptomyces avermitilis MA-4680] Length = 414

2620.1 Best-BlastP=> >nrprot 91% Identities = 65/88 (73%), Positives = 81/88 (92%) ref|NP_395197.1| putative transposase ORFA [Yersinia pestis CO92] ref|NP_857719.1| low calcium response locus protein S homolog [Yersinia pestis KIM] ref|NP_857914.1| putative IS element protein [Yersinia pestis KIM] sp|Q00931|LCRS_YERPE Low calcium response locus protein S pir|T43562 probable IS element protein - Yersinia pestis plasmid pCD1 gb|AAC27655.1| lcrS gb|AAC62579.1| low calcium response locus protein S homolog [Yersinia pestis KIM] gb|AAC69827.1| putative IS element protein [Yersinia pestis KIM] emb|CAB54940.1| putative transposase ORFA [Yersinia pestis] Length = 88

2622.1 Best-BlastP=> >nrprot 58% Identities = 267/639 (41%), Positives = 378/639 (59%), Gaps = 54/639 (8%) ref|NP_111983.1| Adenine specific DNA methylase (Mod-related) [Thermoplasma volcanium] dbj|BAB60632.1| modification methylase [Thermoplasma volcanium] Length = 616

2624.1 Best-BlastP=> >nrprot 38% Identities = 44/156 (28%), Positives = 71/156 (45%), Gaps = 20/156 (12%) ref|ZP_00023112.1| hypothetical protein [Ralstonia metallidurans] Length = 348

2625.2 Best-BlastP=>>nrprot 58% Identities = 129/264 (48%), Positives = 170/264 (64%), Gaps = 2/264 (0%) gb|AAM08235.1| LvrA [Legionella pneumophila] Length = 289

2626.1 Best-BlastP=>>nrprot 56% Identities = 80/221 (36%), Positives = 124/221 (56%), Gaps = 16/221 (7%) gb|AAM08234.1| putative phage repressor [Legionella pneumophila] Length = 227

2627.1 Best-BlastP=>>nrprot 79% Identities = 300/397 (75%), Positives = 334/397 (84%), Gaps = 5/397 (1%) gb|AAB05678.1| HelB Length = 400

263.1 Best-BlastP=>>nrprot 61% Identities = 259/528 (49%), Positives = 339/528 (64%), Gaps = 12/528 (2%) ref|NP_903600.1| L-aspartate oxidase [Chromobacterium violaceum ATCC 12472] gb|AAQ61592.1| L-aspartate oxidase [Chromobacterium violaceum ATCC 12472] Length = 529

2631.4 Best-BlastP=>>nrprot 94% Identities = 875/974 (89%), Positives = 928/974 (95%) sp|Q48815|HELA_LEGPN Protein helA gb|AAB05679.1| HelA Length = 1052

2637.1 Best-BlastP=>>nrprot No Hits found

2639.1 Best-BlastP=>>nrprot 53% Identities = 52/149 (34%), Positives = 80/149 (53%), Gaps = 14/149 (9%) ref|NP_747492.1| hypothetical protein [Pseudomonas putida KT2440] gb|AAN70956.1|AE016739_9 hypothetical protein [Pseudomonas putida KT2440] Length = 193

264.2 Best-BlastP=>>nrprot 72% Identities = 264/457 (57%), Positives = 333/457 (72%), Gaps = 1/457 (0%) ref|ZP_00066450.1| COG0015: Adenylosuccinate lyase [Microbulbifer degradans 2-40] Length = 459

2643.1 Best-BlastP=>>nrprot 44% Identities = 119/434 (27%), Positives = 193/434 (44%), Gaps = 26/434 (5%) ref|NP_564271.1| expressed protein [Arabidopsis thaliana] gb|AAF79860.1|AC000348_13 TN9.21 [Arabidopsis thaliana] Length = 468

2644.1 Best-BlastP=>>nrprot No Hits found

2645.1 Best-BlastP=>>nrprot 24% Identities = 53/135 (39%), Positives = 80/135 (59%), Gaps = 12/135 (8%) ref|ZP_00014821.1| hypothetical protein [Rhodospirillum rubrum] Length = 149

2646.1 Best-BlastP=>>nrprot 49% Identities = 45/117 (38%), Positives = 63/117 (53%), Gaps = 1/117 (0%) ref|NP_386943.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] emb|CAC47416.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] Length = 253

2647.2 Best-BlastP=>>nrprot 72% Identities = 102/185 (55%), Positives = 138/185 (74%), Gaps = 1/185 (0%) ref|NP_621791.1| 3-Methyladenine DNA glycosylase [Thermoanaerobacter tengcongensis] gb|AAM23395.1| 3-Methyladenine DNA glycosylase [Thermoanaerobacter tengcongensis] Length = 188

2648.2 Best-BlastP=>>nrprot 40% Identities = 98/337 (29%), Positives = 148/337 (43%), Gaps = 67/337 (19%) pir|A42596 major outer membrane protein - Legionella pneumophila gb|AAA25300.1| major outer membrane protein Length = 297

2649.1 Best-BlastP=>>nrprot 45% Identities = 99/375 (26%), Positives = 182/375 (48%), Gaps = 2/375 (0%) ref|ZP_00026377.1| COG0475: Kef-type K+ transport systems, membrane components [Ralstonia metallidurans] Length = 406

2650.1 Best-BlastP=>>nrprot 64% Identities = 199/424 (46%), Positives = 284/424 (66%), Gaps = 14/424 (3%) ref|ZP_00031775.1| COG1253: Hemolysins and related proteins containing CBS domains [Burkholderia fungorum] Length = 427

2652.2 Best-BlastP=>>nrprot 46% Identities = 119/354 (33%), Positives = 193/354 (54%), Gaps = 6/354 (1%) gb|AAM00606.1| unknown [Legionella pneumophila] Length = 421

2653.1 Best-BlastP=>>nprot No Hits found

2654.1 Best-BlastP=>>nprot No Hits found

2655.1 Best-BlastP=>>nprot 50% Identities = 35/105 (33%), Positives = 56/105 (53%), Gaps = 6/105 (5%) dbj|BAC93400.1| conserved hypothetical protein [Vibrio vulnificus YJ016] Length = 142

2657.3 Best-BlastP=>>nprot 61% Identities = 324/677 (47%), Positives = 455/677 (67%), Gaps = 12/677 (1%) ref|ZP_00054877.1| COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Magnetospirillum magnetotacticum] Length = 1158

2659.2 Best-BlastP=>>nprot 32% Identities = 34/116 (29%), Positives = 54/116 (46%), Gaps = 12/116 (10%) ref|NP_052947.1| prepropilin [Plasmid R100] sp|P14494|PIL5_ECOLI FIMBRIAL PROTEIN PRECURSOR (PILIN) pir|YQECCR1 fimbrial protein precursor - Escherichia coli plasmid R100-1 gb|AAA92754.1| pilin dbj|BAA78851.1| prepropilin [Plasmid R100] Length = 119

2660.1 Best-BlastP=>>nprot 42% Identities = 24/86 (27%), Positives = 41/86 (47%) sp|P12058|TRAL_SALT TRAL PROTEIN pir|C25161 tral protein - Salmonella typhimurium plasmid pED208 gb|AAA25608.1| Tral protein [Plasmid pED208] gb|AAM90704.1| Tral [Salmonella typhi] Length = 101

2661.2 Best-BlastP=>>nprot 45% Identities = 44/183 (24%), Positives = 85/183 (46%) ref|NP_932206.1| putative conjugative transfer protein TraE [Vibrio vulnificus YJ016] dbj|BAC97729.1| putative conjugative transfer protein TraE [Vibrio vulnificus YJ016] Length = 200

2662.2 Best-BlastP=>>nprot 45% Identities = 72/242 (29%), Positives = 109/242 (45%), Gaps = 19/242 (7%) ref|NP_7625387.1| Unknown [Vibrio vulnificus CMCP6] gb|AAQ07577.1|AE016810_80 Unknown [Vibrio vulnificus CMCP6] Length = 247

2665.1 Best-BlastP=>>nprot No Hits found

2666.1 Best-BlastP=>>nprot No Hits found

2667.1 Best-BlastP=>>nprot No Hits found

2669.2 Best-BlastP=>>nprot 20% Identities = 36/154 (23%), Positives = 71/154 (46%), Gaps = 6/154 (3%) ref|XP_223341.2| similar to KIAA0635 gene product [Rattus norvegicus] Length = 1266

267.3 Best-BlastP=>>nprot 68% Identities = 167/307 (54%), Positives = 216/307 (70%), Gaps = 5/307 (1%) ref|NP_820081.1| tRNA delta(2)-isopentenylpyrophosphate transferase [Coxiella burnetii RSA 493] Length = 311

2670.1 Best-BlastP=>>nprot 16% Identities = 43/143 (30%), Positives = 70/143 (48%), Gaps = 6/143 (4%) ref|NP_842098.1| possible flagellar hook-length control protein [Nitrosomonas europaea ATCC 19718] emb|CAD85999.1| possible flagellar hook-length control protein [Nitrosomonas europaea ATCC 19718] Length = 381

2671.1 Best-BlastP=>>nprot 98% Identities = 203/208 (97%), Positives = 205/208 (98%) sp|P37033|YAC1_LEGPN Hypothetical 23.7 kDa protein in ACN 5'region pir|A48642 hypothetical protein (acn 5' region) - Legionella pneumophila gb|AAA25294.1| putative Length = 208

2674.1 Best-BlastP=>>nprot 99% Identities = 885/891 (99%), Positives = 889/891 (99%) sp|P37032|ACON_LEGPN Aconitase hydratase (Citrate hydro-lyase) (Aconitase) (Major) gb|AAA25295.1| aconitase Length = 891

2677.2 Best-BlastP=>>nprot 70% Identities = 231/451 (51%), Positives = 328/451 (72%), Gaps = 1/451 (0%) ref|NP_820994.1| amino acid transporter [Coxiella burnetii RSA 493] gb|AAQ091508.1| amino acid transporter [Coxiella burnetii RSA 493] Length = 476

268.1 Best-BlastP=>>nrprot 63% Identities = 39/66 (59%), Positives = 45/66 (68%), Gaps = 2/66 (3%) ref|NP_643775.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM38311.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]

2680.1 Best-BlastP=>>nrprot 56% Identities = 93/186 (50%), Positives = 128/186 (68%) ref|NP_819966.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAC090480.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 72

2682.1 Best-BlastP=>>nrprot 30% Identities = 76/390 (19%), Positives = 169/390 (43%), Gaps = 77/390 (19%) ref|NP_703923.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD50535.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 947

2683.3 Best-BlastP=>>nrprot 64% Identities = 253/483 (52%), Positives = 321/483 (66%), Gaps = 1/483 (0%) ref|NP_791659.1| succinyl/glutamic semialdehyde dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO55354.1| succinyl/glutamic semialdehyde dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000] Length = 488

2685.2 Best-BlastP=>>nrprot 32% Identities = 47/192 (24%), Positives = 86/192 (44%), Gaps = 4/192 (2%) ref|ZP_00031024.1| COG0421: Spermidine synthase [Burkholderia fungorum] Length = 252

2688.2 Best-BlastP=>>nrprot No Hits found

269.1 Best-BlastP=>>nrprot 63% Identities = 159/347 (45%), Positives = 224/347 (64%), Gaps = 2/347 (0%) ref|NP_820979.1| heptosyl transferase, glycosyltransferase family 9 protein [Coxiella burnetii RSA 493] gb|AAO91493.1| heptosyl transferase, glycosyltransferase family 9 protein [Coxiella burnetii RSA 493] Length = 351

2690.2 Best-BlastP=>>nrprot No Hits found

2695.2 Best-BlastP=>>nrprot 45% Identities = 55/141 (39%), Positives = 89/141 (63%), Gaps = 6/141 (4%) gb|AAN86353.1| unknown [Listonella pelagia] Length = 195

2696.2 Best-BlastP=>>nrprot 70% Identities = 241/483 (49%), Positives = 342/483 (70%), Gaps = 10/483 (2%) ref|ZP_00117991.1| COG0433: Predicted ATPase [Cytophaga hutchinsonii] Length = 517

2698.1 Best-BlastP=>>nrprot 69% Identities = 64/127 (50%), Positives = 89/127 (70%) ref|NP_5222810.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD18400.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 127

27.1 Best-BlastP=>>nrprot 37% Identities = 41/149 (27%), Positives = 82/149 (55%), Gaps = 2/149 (1%) ref|NP_644250.1| hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM38786.1| hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 211

270.1 Best-BlastP=>>nrprot 61% Identities = 125/278 (44%), Positives = 170/278 (61%), Gaps = 14/278 (5%) gb|AAH53853.1| MGC16638 protein [Homo sapiens] Length = 291

2700.2 Best-BlastP=>>nrprot 45% Identities = 112/367 (30%), Positives = 187/367 (50%), Gaps = 6/367 (1%) ref|NP_907216.1| PUTATIVE EFFLUX PROTEIN [Wolinella succinogenes] emb|CAE10116.1| PUTATIVE EFFLUX PROTEIN [Wolinella succinogenes] Length = 397

2702.2 Best-BlastP=>>nrprot 56% Identities = 103/291 (35%), Positives = 165/291 (56%), Gaps = 7/291 (2%) ref|NP_799583.1| putative transcriptional regulator [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61416.1| putative transcriptional regulator [Vibrio parahaemolyticus] Length = 289

2704.4 Best-BlastP=>nrprot 45%
protein fixL [Pirellula sp.] emb|CAD73291.1| probable sensor protein fixL [Pirellula sp.] Length = 651

2705.3 Best-BlastP=>nrprot 61%
Identities = 173/388 (44%), Positives = 239/388 (61%), Gaps = 16/388 (4%) ref|ZP_00054896.1| COG3287:
Uncharacterized conserved protein [Magnetospirillum magnetotacticum] Length = 376

2706.2 Best-BlastP=>nrprot 24%
Identities = 72/75 (96%), Positives = 72/75 (96%) gb|AAC61480.1| unknown [Legionella pneumophila] Length = 77

2709.1 Best-BlastP=>nrprot 64%
Identities = 158/320 (49%), Positives = 212/320 (66%), Gaps = 2/320 (0%) ref|NP_245036.1| unknown [Pasteurella multocida] gb|AAK02183.1| unknown [Pasteurella multocida] Length = 337

271.1 Best-BlastP=>nrprot 29%
Identities = 45/133 (33%), Positives = 79/133 (59%), Gaps = 3/133 (2%) ref|NP_149698.1| 235L [Invertebrate iridescent virus 6] gb|AAK82096.1|AF303741_235 235L [Chilo iridescent virus] Length = 265

2712.1 Best-BlastP=>nrprot 29%
Identities = 57/175 (32%), Positives = 81/175 (46%), Gaps = 13/175 (7%) ref|NP_231966.1| hypothetical protein VC2335 [Vibrio cholerae O1 biovar eltor str. N16961] pir|E82090 hypothetical protein VC2335 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95479.1| hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 195

2713.2 Best-BlastP=>nrprot 52%
Identities = 107/319 (33%), Positives = 178/319 (55%), Gaps = 14/319 (4%) ref|NP_441143.1| unknown protein [Synechocystis sp. PCC 6803] sp|P73771|YB64_SYNY3 Hypothetical transport protein sll1164 pir|S74862 hypothetical protein sll1164 - Synechocystis sp. (strain PCC 6803) dbj|BAA17823.1| ORF_ID:sll1164~unknown protein [Synechocystis sp. PCC 6803] Length = 349

2717.1 Best-BlastP=>nrprot No Hits found

2718.1 Best-BlastP=>nrprot 71%
Identities = 254/438 (57%), Positives = 324/438 (73%), Gaps = 10/438 (2%) ref|NP_220059.1| Hexosaminoglycan Transport [Chlamydia trachomatis] sp|O84548|UHPT_CHLTR Probable hexose phosphate transport protein pir|A71501 probable hexosaminoglycan transport - Chlamydia trachomatis (serotype D, strain UW3/Cx) gb|AAC618146.1| Hexosaminoglycan transport [Chlamydia trachomatis] Length = 456

2721.3 Best-BlastP=>nrprot 67%
Identities = 383/736 (52%), Positives = 502/736 (68%), Gaps = 10/736 (1%) ref|ZP_00095016.1| COG0022:
Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta aromaticivorans] Length = 738

2724.3 Best-BlastP=>nrprot 45%
Identities = 96/404 (23%), Positives = 177/404 (43%), Gaps = 76/404 (18%) ref|ZP_00083983.1| hypothetical protein [Pseudomonas fluorescens PH-1] Length = 524

2725.1 Best-BlastP=>nrprot 62%
Identities = 39/75 (52%), Positives = 56/75 (74%) ref|NP_420714.1| flhB-related protein [Caulobacter crescentus CB15] pir|F87485 flhB-related protein [imported] - Caulobacter crescentus gb|AAK23882.1| flhB-related protein [Caulobacter crescentus CB15] Length = 87

2726.1 Best-BlastP=>nrprot No Hits found

2727.2 Best-BlastP=>nrprot 16%
Identities = 70/336 (20%), Positives = 147/336 (43%), Gaps = 50/336 (14%) gb|AAL99918.1|AF432211_1 CLL-associated antigen KW-111 [Homo sapiens] Length = 460

2728.1	Best-BlastP=>nrprot 61% Identities = 49/1103 (47%), Positives = 65/1103 (63%) ref NP_903992.1 conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb AAQ61981.1 conserved hypothetical protein [Chromobacterium violaceum ATCC 12472]
Length = 117	
273.1	Best-BlastP=>nrprot No Hits found
2730.1	Best-BlastP=>nrprot No Hits found
2732.1	Best-BlastP=>nrprot No Hits found
2733.1	Best-BlastP=>nrprot 58% Identities = 133/345 (38%), Positives = 206/345 (59%), Gaps = 12/345 (3%) ref NP_437388.1 putative conserved membrane-anchored protein [Sinorhizobium meliloti] pir H95947 probable conserved membrane-anchored protein SMb21182 [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb CAC49248.1 putative conserved membrane-anchored protein [Sinorhizobium meliloti] Length = 394
2737.2	Best-BlastP=>nrprot No Hits found
2738.2	Best-BlastP=>nrprot 43% Identities = 55/255 (21%), Positives = 112/255 (43%), Gaps = 16/255 (6%) ref NP_900118.1 probable ABC transporter system permease protein [Chromobacterium violaceum ATCC 12472] gb AAQ58126.1 probable ABC transport system permease protein [Chromobacterium violaceum ATCC 12472] Length = 257
2739.3	Best-BlastP=>nrprot 50% Identities = 67/256 (26%), Positives = 115/256 (44%), Gaps = 51/256 (19%) ref NP_518722.1 PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb CAD14131.1 PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 547
2741.2	Best-BlastP=>nrprot 52% Identities = 20/40 (50%), Positives = 24/40 (60%) ref NP_907600.1 hypothetical protein WS1440 [Wolinella succinogenes] emb CAE10500.1 hypothetical protein [Wolinella succinogenes] Length = 42
2742.2	Best-BlastP=>nrprot 77% Identities = 34/42 (80%), Positives = 34/42 (80%) ref NP_759472.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_759895.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_759901.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760122.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_763326.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_763326.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760021.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760328.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760328.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_76016800_27 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09422.1 AE016800_27 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09428.1 AE016800_33 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09649.1 AE016800_254 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09855.1 AE016801_174 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 43
2743.2	Best-BlastP=>nrprot 82% Identities = 52/66 (78%), Positives = 56/66 (84%) ref NP_759471.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_759894.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_759900.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_759939.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760021.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760123.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760123.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760403.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref NP_760403.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO08317.1 AE016813_69 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09421.1 AE016800_26 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO08998.1 AE016798_158 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09427.1 AE016800_32 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09466.1 AE016800_71 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb AAO09548.1 AE016800_153 Conserved hypothetical protein [Vibrio vulnificus CMCP6]

2747.1 Best-BlastP=> >nrprot 62% Identities = 129/323 (39%), Positives = 203/323 (62%), Gaps = 4/323 (1%) ref|NP_384238.1| PUTATIVE ADENOSINE DEAMINASE PROTEIN [Sinorhizobium meliloti] sp|Q92T48|ADD_RHME Adenosine deaminase (Adenosine aminohydrolase) embl|CAC41519.1| PUTATIVE ADENOSINE DEAMINASE PROTEIN [Sinorhizobium meliloti] Length = 324

2748.1 Best-BlastP=> >nrprot No Hits found

2749.4 Best-BlastP=> >nrprot 67% Identities = 204/415 (49%), Positives = 283/415 (68%) ref|NP_819070.1| phosphate transporter family protein [Coxiella burnetii RSA 493] Length = 417

2751.1 Best-BlastP=> >nrprot 48% Identities = 83/226 (36%), Positives = 125/226 (55%), Gaps = 5/226 (2%) ref|NP_212383.1| phosphatidyltransferase [Borrelia burgdorferi] pir|A70131 phosphatidyltransferase homolog - Lyme disease spirochete gb|AAB91497.1| phosphatidyltransferase [Borrelia burgdorferi B31] Length = 234

2752.1 Best-BlastP=> >nrprot 49% Identities = 53/167 (31%), Positives = 81/167 (48%), Gaps = 14/167 (8%) ref|NP_819930.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 169

2753.1 Best-BlastP=> >nrprot No Hits found

2754.2 Best-BlastP=> >nrprot 72% Identities = 109/184 (59%), Positives = 134/184 (72%) ref|NP_820271.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAC90785.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 185

2755.1 Best-BlastP=> >nrprot 29% Identities = 102/461 (22%), Positives = 198/461 (42%), Gaps = 56/461 (12%) ref|NP_788908.1| CG33206-PB [Drosophila melanogaster] gb|AAF48467.2| CG33206-PB [Drosophila melanogaster] Length = 1208

2757.1 Best-BlastP=> >nrprot 73% Identities = 78/148 (52%), Positives = 110/148 (74%) ref|ZP_00125250.1| COG0359: Ribosomal protein L9 [Pseudomonas syringae pv. syringae B728a] ref|NP_794663.1| ribosomal protein L9 [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58358.1| ribosomal protein L9 [Pseudomonas syringae pv. tomato str. DC3000] Length = 148

2759.1 Best-BlastP=> >nrprot 40% Identities = 74/283 (26%), Positives = 130/283 (45%), Gaps = 14/283 (4%) ref|NP_819885.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90399.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 299

276.1 Best-BlastP=> >nrprot 25% Identities = 20/25 (80%), Positives = 20/25 (80%), Gaps = 1/25 (4%) ref|NP_084281.1| RIKEN cDNA A030005K14 [Mus musculus] dbj|BAB32176.1| unnamed protein product [Mus musculus] Length = 122

2760.1 Best-BlastP=> >nrprot 85% Identities = 53/75 (70%), Positives = 65/75 (86%) ref|NP_240367.1| 30S ribosomal protein S18 [Buchnera aphidicola str. APS (Acyrthosiphon pisum)] sp|P57626|RS18_BUCA1 30S ribosomal protein S18 pir|E84995 30S ribosomal protein S18 [imported] - Buchnera sp. (strain APS) dbj|BAB13253.1| 30S ribosomal protein S18 [Buchnera aphidicola str. APS (Acyrthosiphon pisum)] = 75 Length = 75

2761.1 Best-BlastP=> >nrprot 75% Identities = 70/107 (65%), Positives = 85/107 (79%) ref|NP_903310.1| 30S ribosomal protein S6 [Chromobacterium violaceum ATCCC 12472] Length = 124

2763.2 Best-BlastP=> >nrprot No Hits found

2765.2 Best-BlastP=> >nrprot 33% Identities = 48/222 (21%), Positives = 99/222 (44%), Gaps = 21/222 (9%) ref|NP_106991.1| unknown protein [Mesorhizobium loti] dbj|BAB52777.1| unknown protein [Mesorhizobium loti] Length = 328

2767.1 Best-BlastP=> >nrprot No Hits found

2769.2 Best-BlastP=> >nrprot 53% Identities = 203/594 (34%), Positives = 317/594 (53%), Gaps = 26/594 (4%) ref|NP_2666737.1| hypothetical protein [Lactococcus lactis subsp. lactis] pir|E866997 conserved hypothetical protein yfhG [imported] - Lactococcus lactis subsp. lactis (strain IL1403) gb|AAK04679.1|AE006291_13 conserved hypothetical protein [Lactococcus lactis subsp. lactis] Length = 598

2770.1 Best-BlastP=> >nrprot 41% Identities = 60/196 (30%), Positives = 99/196 (50%), Gaps = 18/196 (9%) ref|NP_436484.1| hypothetical protein [Sinorhizobium meliloti] pir|F95416 hypothetical protein SMA2299 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA gb|AAK65896.1| hypothetical protein [Sinorhizobium meliloti] Length = 308

2770.1 Best-BlastP=> >nrprot 65% Identities = 114/240 (47%), Positives = 153/240 (63%), Gaps = 14/240 (5%) ref|NP_867184.1| short chain alcohol dehydrogenase-like [Pirellula sp.] emb|CAD74729.1| short chain alcohol dehydrogenase-like [Pirellula sp.] Length = 247

2771.2 Best-BlastP=> >nrprot 66% Identities = 205/386 (53%), Positives = 260/386 (67%), Gaps = 1/386 (0%) ref|NP_355900.1| AGR_L_236p [Agrobacterium tumefaciens] ref|NP_535243.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|C98145 hypothetical protein AGR_L_236 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AI3142 conserved hypothetical protein Atu4765 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK88685.1| AGR_L_236p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL45559.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 507

2772.1 Best-BlastP=> >nrprot 51% Identities = 40/131 (30%), Positives = 71/131 (54%), Gaps = 12/131 (9%) ref|NP_469941.1| lin0598 [Listeria innocua] pir|AF1507 hypothetical protein lin0598 [imported] - Listeria innocua (strain innocua) Length = 138

2774.1 Best-BlastP=> >nrprot 69% Identities = 152/286 (53%), Positives = 204/286 (71%) ref|NP_697358.1| transcriptional regulator, LysR family [Brucella suis 1330] gb|AN29273.1|AE014344_8 transcriptional regulator, LysR family [Brucella suis 1330] Length = 296

2775.1 Best-BlastP=> >nrprot 50% Identities = 31/52 (59%), Positives = 36/52 (69%), Gaps = 3/52 (5%) ref|ZP_00021959.1| COG3024: Uncharacterized protein conserved in bacteria [Ralstonia metallidurans] Length = 63

2777.1 Best-BlastP=> >nrprot 64% Identities = 174/343 (50%), Positives = 232/343 (67%), Gaps = 5/343 (1%) ref|NP_780210.1| phosphoribosylaminoimidazole carboxylase, ATPase subunit [Xylella fastidiosa Temecula1] gb|AAO29859.1| Length = 394

2778.2 Best-BlastP=> >nrprot 82% Identities = 113/160 (70%), Positives = 138/160 (86%) ref|ZP_00066669.1| COG0041: Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase [Microbulbifer degradans 2-40] Length = 168

278.3 Best-BlastP=> >nrprot 51% Identities = 218/623 (34%), Positives = 331/623 (53%), Gaps = 47/623 (7%) ref|NP_070765.1| phosphoribosylformylglycaminidine synthase II (purl) [Archaeoglobus fulgidus DSM 4304] sp|O28339|PURL_ARCFU

2780.2 Best-BlastP=> >nrprot 57% Identities = 116/273 (42%), Positives = 162/273 (59%), Gaps = 3/273 (1%) ref|NP_925031.1| hypothetical protein g|r2085 [Gloeobacter violaceus] dbj|BAC90026.1| g|r2085 [Gloeobacter violaceus] Length = 288

2781.1 Best-BlastP=> >nrprot 70% Identities = 49/103 (47%), Positives = 75/103 (72%) ref|NP_213586.1| putative protein [Aequifex aeolicus] pir|F70374 hypothetical protein aq_862 - Aequifex aeolicus gb|AAC06993.1| putative protein [Aequifex aeolicus] VF5] Length = 109

2784.3 Best-BlastP=>>nrprot 49% Identities = 36/80 (45%), Positives = 52/80 (65%) ref|NP_931069.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE16236.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii TTO1] Length = 124

2785.1 Best-BlastP=>>nrprot 71% Identities = 153/265 (57%), Positives = 202/265 (76%), Gaps = 1/265 (0%) ref|NP_819150.1| nicotinate-nucleotide pyrophosphorylase [Coxiella burnetii RSA 493] Length = 274

2788.1 Best-BlastP=>>nrprot 54% Identities = 158/473 (33%), Positives = 263/473 (55%), Gaps = 39/473 (8%) ref|NP_485346.1| Na+/H+ antiporter [Nostoc sp. PCC 7120] pir|JAD1969 Na+/H+ antiporter [Imported] - Nostoc sp. (strain PCC 7120) dbj|BAB73260.1| Na+/H+ antiporter [Nostoc sp. PCC 7120] Length = 470

2791.1 Best-BlastP=>>nrprot 82% Identities = 537/779 (68%), Positives = 655/779 (84%), Gaps = 5/779 (0%) ref|NP_310436.1| phosphoenolpyruvate synthase [Escherichia coli O157:H7] pir|A90930 phosphoenolpyruvate synthase [Imported] - Escherichia coli (strain RIMD 0509952) dbj|BAB35832.1| phosphoenolpyruvate synthase [Escherichia coli O157:H7] Length = 792

2792.1 Best-BlastP=>>nrprot No Hits found

2793.1 Best-BlastP=>>nrprot 50% Identities = 100/343 (29%), Positives = 170/343 (49%), Gaps = 28/343 (8%) ref|NP_233263.1| hydrolase, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir|E82406 probable hydrolase VCA0877 [Imported] - Vibrio cholerae (strain serogroup O1) gb|AAF96775.1| hydrolase, putative [Vibrio cholerae O1 biovar eltor str. N16961] Length = 358

2794.2 Best-BlastP=>>nrprot 44% Identities = 152/532 (28%), Positives = 250/532 (46%), Gaps = 31/532 (5%) ref|ZP_00029700.1| COG1960: Acyl-CoA dehydrogenases [Burkholderia fungorum] Length = 587

2795.1 Best-BlastP=>>nrprot 87% Identities = 60/88 (68%), Positives = 78/88 (88%) ref|NP_395197.1| putative transposase ORFA [Yersinia pestis CO92] ref|NP_857719.1| low calcium response locus protein S homolog [Yersinia pestis] KIM] ref|NP_857794.1| putative IS element protein [Yersinia pestis KIM] sp|Q00931|LCRS_YERPE Low calcium response locus protein S pir|T43562 probable IS element protein - Yersinia pestis plasmid pCD1 gb|AA27655.1| IcrS pir|AAC62579.1| low calcium response locus protein S homolog [Yersinia pestis] KIM] gb|AAC69827.1| putative IS element protein [Yersinia pestis KIM] emb|CAB54940.1| putative transposase ORFA [Yersinia pestis] Length = 88

2799.1 Best-BlastP=>>nrprot 67% Identities = 71/126 (56%), Positives = 91/126 (72%) ref|NP_867058.1| aspartate 1-decarboxylase [Shewanella oneidensis MR-1] emb|CAD74603.1| aspartate 1-decarboxylase [Pirellula sp.] Length = 156

2800.1 Best-BlastP=>>nrprot 66% Identities = 136/258 (52%), Positives = 172/258 (66%), Gaps = 3/258 (1%) ref|NP_719181.1| dimethyladenosine transferase [Shewanella oneidensis MR-1] sp|Q8EB93|KSGA_SHEON Dimethyladenosine transferase (S-adenosylmethionine-6-N'-adenosyl(rRNA) dimethyltransferase) (16S rRNA dimethyltransferase) (High level kasugamycin resistance protein KsgA) (Kasugamycin dimethyltransferase) gb|AAN56625.1|AE015799.12 dimethyladenosine transferase [Shewanella oneidensis MR-1] Length = 268

2804.1 Best-BlastP=>>nrprot 63% Identities = 232/443 (52%), Positives = 286/443 (64%), Gaps = 2/443 (0%) ref|NP_629805.1| putative 4-aminobutyrate aminotransferase [Streptomyces coelicolor A3(2)] pir|T35794 probable 4-aminobutyrate aminotransferase - Streptomyces coelicolor emb|CAA20213.1| putative 4-aminobutyrate aminotransferase [Streptomyces coelicolor A3(2)] Length = 444

2806.1 Best-BlastP=>>nrprot 76% Identities = 118/196 (60%), Positives = 153/196 (78%) ref[NP_249757.1] probable short-chain dehydrogenase [Pseudomonas aeruginosa PA01] pir|[H83512 probable short-chain dehydrogenase PA1066 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|[AAG04455.1|AE004538_7 probable short-chain dehydrogenase [Pseudomonas aeruginosa PA01] Length = 218

2807.1 Best-BlastP=>>nrprot 71% Identities = 54/113 (47%), Positives = 81/113 (71%), Gaps = 5/113 (4%) ref[NP_798658_1| arsenate reductase [Vibrio parahaemolyticus RIMD 2210633] db|[BAC60542.1| arsenate reductase [Vibrio parahaemolyticus] Length = 116

2808.1 Best-BlastP=>>nrprot 60% Identities = 39/83 (46%), Positives = 56/83 (67%), Gaps = 1/83 (1%) gb|[AAL07519.1| RNA-binding protein precursor [Solanum tuberosum] Length = 339

2810.1 Best-BlastP=>>nrprot 48% Identities = 130/457 (28%), Positives = 218/457 (47%), Gaps = 24/457 (5%) emb|CAD48863.1| EefC outer membrane protein [Enterobacter aerogenes] Length = 454

2811.2 Best-BlastP=>>nrprot 25% Identities = 43/179 (24%), Positives = 89/179 (49%), Gaps = 4/179 (2%) ref[NP_820323.1| conserved domain protein [Coxiella burnetii RSA 493] gb|[AAO90837.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 377

2815.2 Best-BlastP=>>nrprot 9% Identities = 31/89 (34%), Positives = 54/89 (60%) ref[NP_819452.1| hypothetical protein [Coxiella burnetii RSA 493] gb|[AO89966.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 262

2816.2 Best-BlastP=>>nrprot 50% Identities = 191/730 (26%), Positives = 361/730 (49%), Gaps = 43/730 (5%) ref[ZP_00055987.1| COG0659: Sulfate permease and related transporters (MFS superfamily) [Magnetospirillum magnetotacticum] Length = 733

2818.1 Best-BlastP=>>nrprot 61% Identities = 155/372 (41%), Positives = 219/372 (58%), Gaps = 37/372 (9%) gb|[AK97454.1|AF388182_2 alkane-1-monooxygenase [Rhodococcus sp. Q15] Length = 408

2822.1 Best-BlastP=>>nrprot 52% Identities = 58/179 (32%), Positives = 103/179 (57%), Gaps = 12/179 (6%) ref[NP_900154.1| probable type IV prepilin [Chromobacterium violaceum ATCC 12472] gb|[AAQ58161.1| probable type IV prepilin [Chromobacterium violaceum ATCC 12472] Length = 185

2820.1 Best-BlastP=>>nrprot 64% Identities = 145/273 (53%), Positives = 183/273 (67%), Gaps = 4/273 (1%) ref[NP_439796.1| hypothetical protein [Haemophilus influenzae Rd] sp|[P45298|YRAL_HAEIN Hypothetical protein H1654 pir|[A64174 hypothetical protein H1654 - Haemophilus influenzae (strain Rd) KW20] gb|[AAC23298.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 283

2824.1 Best-BlastP=>>nrprot 72% Identities = 83/138 (60%), Positives = 102/138 (73%) ref[NP_254240.1| ATP synthase epsilon chain [Pseudomonas aeruginosa PA01] sp|[Q9HT21|ATPE_PSEAE ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) pir|[B82952 ATP synthase epsilon chain PA5553 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|[AAG08938.1|AE004967_9 ATP synthase epsilon chain [Pseudomonas aeruginosa PAO1] Length = 141

2826.1 Best-BlastP=>>nrprot 42% Identities = 110/540 (20%), Positives = 217/540 (40%), Gaps = 94/540 (17%) ref[ZP_00144200.1| EXONUCLEASE SBCC [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb|[EAA24200.1| EXONUCLEASE SBCC [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 921

2827.3 Best-BlastP=>>nrprot No Hits found

2828.3 Best-BlastP=> >nrprot 72% Identities = 29/52 (55%), Positives = 36/52 (69%), Gaps = 2/52 (3%) ref|NP_885117.1| phosphatidylserine decarboxylase proenzyme [Bordetella parapertussis] emb|CAE38217.1| phosphatidylserine decarboxylase proenzyme [Bordetella parapertussis] Length = 328

283.1 Best-BlastP=> >nrprot 47% Identities = 52/142 (36%), Positives = 86/142 (60%), Gaps = 8/142 (5%) ref|NP_900149.1| probable type-4 fimbrial biogenesis protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58156.1| probable type-4 fimbrial biogenesis protein [Chromobacterium violaceum ATCC 12472] Length = 159

2830.3 Best-BlastP=> >nrprot No Hits found

2831.1 Best-BlastP=> >nrprot 47% Identities = 71/219 (32%), Positives = 106/219 (48%), Gaps = 10/219 (4%) ref|NP_801239.1| transcriptional regulator, LuxR family [Vibrio parahaemolyticus] RIMD 2210633] dbj|BAC63072.1| transcriptional regulator, LuxR family [Vibrio parahaemolyticus] Length = 251

2833.1 Best-BlastP=> >nrprot 56% Identities = 125/332 (37%), Positives = 186/332 (56%), Gaps = 22/332 (6%) ref|NP_956686|CPDP_VIBF1 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE PRECURSOR (PDEASE) (3':5'-CNP) pir|A40602 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - Vibrio fischeri gb|AAA27513.1| cpdP Length = 330

2835.1 Best-BlastP=> >nrprot 70% Identities = 151/281 (53%), Positives = 200/281 (71%), Gaps = 1/281 (0%) ref|NP_754359.1| Putative 3-hydroxyacyl-CoA dehydrogenase [Escherichia coli CFT073] gb|AAN80926.1|AE016762_179 Putative 3-hydroxyacyl-CoA dehydrogenase [Escherichia coli CFT073] Length = 289

2838.1 Best-BlastP=> >nrprot 67% Identities = 176/365 (48%), Positives = 253/365 (69%) ref|ZP_00110259.1| COG1960: Acyl-CoA dehydrogenases [Nostoc punctiforme] Length = 395

284.2 Best-BlastP=> >nrprot 57% Identities = 128/361 (35%), Positives = 203/361 (56%), Gaps = 24/361 (6%) ref|NP_900150.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58157.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 354

2840.1 Best-BlastP=> >nrprot 62% Identities = 225/502 (44%), Positives = 316/502 (62%), Gaps = 9/502 (1%) pir|T44808 mycosubtilin synthetase mycC [Imported] - Bacillus subtilis gb|AAF08797.1|AF184956_4 MycC [Bacillus subtilis] Length = 2609

2841.4 Best-BlastP=> >nrprot 58% Identities = 175/439 (39%), Positives = 259/439 (58%), Gaps = 14/439 (3%) ref|ZP_00111186.1| COG3321: Polyketide synthase modules and related proteins [Nostoc punctiforme] Length = 1853

2847.4 Best-BlastP=> >nrprot No Hits found

2848.4 Best-BlastP=> >nrprot No Hits found

2849.1 Best-BlastP=> >nrprot No Hits found

2858.1 Best-BlastP=> >nrprot 28% Identities = 23/33 (69%), Positives = 24/33 (72%) pir|A44803 pG1 protein - human (fragment) Length = 75

2859.2 Best-BlastP=> >nrprot 76% Identities = 254/393 (64%), Positives = 308/393 (78%) ref|NP_716935.1| tyrosyl-tRNA synthetase [Shewanella oneidensis MR-1] gb|AN54380.1|AE015575_6 tyrosyl-tRNA synthetase [Shewanella oneidensis MR-1] Length = 398

286.2 Best-BlastP=> >nrprot 48% Identities = 48/165 (29%), Positives = 83/165 (50%), Gaps = 18/165 (10%) ref|NP_900151.1| hypothetical protein CV0481 [Chromobacterium violaceum ATCC 12472] gb|AAQ58158.1| hypothetical protein CV0481 [Chromobacterium violaceum ATCC 12472] Length = 168

2861.1 Best-BlastP=> >nrprot 67% Identities = 131/262 (50%), Positives = 185/262 (70%), Gaps = 1/262 (0%) ref|ZP_00068001.1| COG3220: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] Length = 290

2862.1 Best-BlastP=> >nrprot 52% Identities = 142/396 (35%), Positives = 210/396 (53%), Gaps = 7/396 (1%) ref|NP_349992.1| Dipeptidyl aminopeptidase/acylaminocyl-peptidase related protein [Clostridium acetobutylicum] pir|[A97318 dipeptidyl aminopeptidase/acylaminocyl-peptidase related protein [imported] - Clostridium acetobutylicum gb|AAK81332.1|AE007837_10 Dipeptidyl aminopeptidase/acylaminocyl-peptidase related protein [Clostridium acetobutylicum] Length = 400

2863.1 Best-BlastP=> >nrprot 35% Identities = 46/117 (39%), Positives = 68/117 (58%), Gaps = 4/117 (3%) ref|ZP_00008611.1| COG0845: Membrane-fusion protein [Rhodopseudomonas palustris] Length = 267

2866.1 Best-BlastP=> >nrprot 78% Identities = 276/431 (64%), Positives = 347/431 (80%), Gaps = 1/431 (0%) ref|NP_901043.1| probable oxidoreductase [Chromobacterium violaceum ATCC 12472] gb|AAQ59048.1| probable oxidoreductase [Chromobacterium violaceum ATCC 12472] Length = 438

2868.1 Best-BlastP=> >nrprot 60% Identities = 247/585 (42%), Positives = 357/585 (61%), Gaps = 15/585 (2%) ref|NP_820704.1| thiol:disulfide interchange protein DsbD [Coxiella burnetii RSA 493] Length = 584

2869.1 Best-BlastP=> >nrprot 98% Identities = 96/96 (100%), Positives = 96/96 (100%) ref|P26879|CH10_LEGPN 10 kDa chaperonin (Protein Cpn10) (groES protein) (Heat shock protein A) pir|[B41468 heat shock protein groES - Legionella pneumophila gb|AAA25297.1| htpA = 96

2873.1 Best-BlastP=> >nrprot 40% Identities = 66/274 (24%), Positives = 130/274 (47%), Gaps = 16/274 (5%) ref|NP_692096.1| hypothetical protein [Oceanobacillus iheyensis HTE831] dbj|BAC13131.1| hypothetical conserved protein [Oceanobacillus iheyensis HTE831] Length = 314

2874.1 Best-BlastP=> >nrprot 59% Identities = 111/225 (49%), Positives = 155/225 (68%), Gaps = 1/225 (0%) ref|NP_6621190.1| hypothetical protein [Chlorobium tepidum TLS] gb|AAM72532.1| hypothetical protein [Chlorobium tepidum TLS] Length = 232

2877.2 Best-BlastP=> >nrprot 49% Identities = 71/206 (34%), Positives = 109/206 (52%), Gaps = 3/206 (1%) ref|NP_902629.1| hypothetical protein CV2959 [Chromobacterium violaceum ATCC 12472] gb|AAQ60627.1| hypothetical protein CV2959 [Chromobacterium violaceum ATCC 12472] Length = 214

2878.2 Best-BlastP=> >nrprot 98% Identities = 226/230 (98%), Positives = 228/230 (99%) gb|AAK00284.1|AF288536_6 possible transcriptional regulatory protein [Legionella longbeachae] Length = 230

2879.3 Best-BlastP=> >nrprot 96% Identities = 419/444 (94%), Positives = 430/444 (96%), Gaps = 2/444 (0%) gb|AAK00283.1|AF288536_5 unknown [Legionella longbeachae] Length = 444

2881.2 Best-BlastP=> >nrprot 93% Identities = 270/302 (89%), Positives = 281/302 (93%), Gaps = 1/302 (0%) gb|AAK00282.1|AF288536_4 unknown [Legionella longbeachae] Length = 302

2882.2 Best-BlastP=> >nrprot 76% Identities = 146/221 (66%), Positives = 175/221 (79%), Gaps = 1/221 (0%) ref|NP_249667.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] ref|ZP_00138566.1| COG0603: Predicted PP-loop superfamily ATPase [Pseudomonas aeruginosa UCBPP-PA14] pir|[E83522 conserved hypothetical protein PA0976 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG04365.1|AE004531_2 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] gb|AAP82946.1| conserved hypothetical protein [Pseudomonas aeruginosa] Length = 224

2884.1 Best-BlastP=> >nrprot No Hits found

2889.2 Best-BlastP=> >nrprot 69% Identities = 72/124 (58%), Positives = 90/124 (72%) ref|NP_719248.1| membrane protein, putative [Shewanella oneidensis MR-1] gb|AAN56692.1|AE015805_1 membrane protein, putative [Shewanella oneidensis MR-1] Length = 127

2891.2 Best-BlastP=> >nrprot 58% Identities = 235/584 (40%), Positives = 355/584 (61%), Gaps = 4/584 (0%) ref|NP_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - *Rickettsia conorii* (strain Malish 7) gb|AAU02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589

2893.2 Best-BlastP=> >nrprot 51% Identities = 263/741 (35%), Positives = 402/741 (54%), Gaps = 32/741 (4%) ref|ZP_00080393.1| hypothetical protein [Geobacter metallireducens] Length = 768

2898.4 Best-BlastP=> >nrprot 61% Identities = 27/72 (37%), Positives = 47/72 (65%) ref|NP_660683.1| acyl-carrier protein [Buchnera aphidicola] str. Sg (Schizaphis graminum)] sp|Q8K9J4|ACP_BUCAP Acyl carrier protein (ACP) gb|AAU67894.1| acyl-carrier protein [Buchnera aphidicola] str. Sg (Schizaphis graminum)] Length = 79

29.1 Best-BlastP=> >nrprot 39% Identities = 26/62 (41%), Positives = 38/62 (61%) gb|AAO43539.1| probable conjugal transfer protein TraD [Rhizobium etli] Length = 71

290.2 Best-BlastP=> >nrprot 58% Identities = 501/1050 (47%), Positives = 679/1050 (64%), Gaps = 57/1050 (5%) ref|NP_900152.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58159.2| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 1040

2900.2 Best-BlastP=> >nrprot 50% Identities = 121/308 (39%), Positives = 170/308 (55%), Gaps = 4/308 (1%) ref|NP_829350.1| 3-oxoacyl-(acyl)-carrier protein) synthase III [Chlamydophila caviae] gpi|AAP05228.1| 3-oxoacyl-(acyl-carrier-protein) synthase III [Chlamydophila caviae] gpi|C

2905.2 Best-BlastP=> >nrprot No Hits found

2906.2 Best-BlastP=> >nrprot 62% Identities = 95/201 (47%), Positives = 127/201 (63%), Gaps = 1/201 (0%) ref|NP_929829.1| Glutathione S-transferase [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE14968.1| Glutathione S-transferase [Photorhabdus luminescens subsp. laumontii TTO1] Length = 335

2908.2 Best-BlastP=> >nrprot No Hits found

2909.1 Best-BlastP=> >nrprot 54% Identities = 137/387 (35%), Positives = 210/387 (54%), Gaps = 25/387 (6%) ref|NP_441897.1| D-alanyl-D-alanine carboxypeptidase [Synechocystis sp. PCC 6803] pir|S76446 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj|BA18575.1| D-alanyl-D-alanine carboxypeptidase [Synechocystis sp. PCC 6803] Length = 400

291.4 Best-BlastP=> >nrprot 79% Identities = 283/419 (67%), Positives = 342/419 (81%) ref|NP_820426.1| NADH dehydrogenase I, F subunit [Coxiella burnetii RSA 493] gb|AAC090940.1| NADH dehydrogenase I, F subunit [Coxiella burnetii RSA 493] Length = 422

2910.1 Best-BlastP=> >nrprot 73% Identities = 272/465 (58%), Positives = 348/465 (74%), Gaps = 1/465 (0%) ref|NP_928701.1| glutamyl-tRNA synthetase, catalytic subunit [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE13694.1| glutamyl-tRNA synthetase, catalytic subunit [Photorhabdus luminescens subsp. laumontii TTO1] Length = 472

2911.3

Best-BlastP=> >nrprot 58% Identities = 47/95 (49%), Positives = 62/95 (65%) ref|NP_931076.1| BolA protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16243.1| BolA protein [Photorhabdus luminescens subsp. laumondii TTO1] Length = 104

2914.1 Best-BlastP=> >nrprot 60% Identities = 90/225 (40%), Positives = 135/225 (60%), Gaps = 15/225 (6%) ref|NP_759151.1| Inactive homolog of metal-dependent proteases [Vibrio vulnificus CMCP6] gbl|AAO08678.1|AE016797_133 Inactive homolog of metal-dependent proteases [Vibrio vulnificus CMCP6] Length = 233

2915.2 Best-BlastP=> >nrprot 8% Identities = 45/199 (22%), Positives = 77/199 (38%), Gaps = 4/199 (2%) ref|NP_497967.1| cyclin-like F-box (3F797) [Caenorhabditis elegans] pir|T24435 hypothetical protein T04A8.13 - Caenorhabditis elegans emb|CAA84732.2| Hypothetical protein T04A8.13 [Caenorhabditis elegans] Length = 791

2916.1 Best-BlastP=> >nrprot No Hits found

2917.1 Best-BlastP=> >nrprot 30% Identities = 44/132 (33%), Positives = 71/132 (53%), Gaps = 11/132 (8%) ref|NP_707288.1| Activator of ProP osmoprotectant transporter [Shigella flexneri 2a str. 301] gbl|AAN42995.1|AE015164_2 Activator of ProP osmoprotectant transporter [Shigella flexneri 2a str. 301] Length = 232

2919.1 Best-BlastP=> >nrprot 55% Identities = 23/55 (41%), Positives = 33/55 (60%), Gaps = 4/55 (7%) ref|NP_768003.1| bsl|BAA25988.1| 24-kDa subunit of Bradyrhizobium japonicum] dbj|BAC46628.1| bsl|BAA25988.1| 24-kDa subunit of Bradyrhizobium japonicum USDA 110] Length = 73

2921.1 Best-BlastP=> >nrprot 69% Identities = 75/152 (49%), Positives = 108/152 (71%), Gaps = 1/152 (0%) dbj|BAA25988.1| 24-kDa subunit of complex I [Homo sapiens] Length = 231

2920.1 Best-BlastP=> >nrprot No Hits found

2921.3 Best-BlastP=> >nrprot 17% Identities = 81/447 (18%), Positives = 193/447 (43%), Gaps = 55/447 (12%) pir|E71606 hypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum) Length = 980

2924.3 Best-BlastP=> >nrprot 61% Identities = 385/477 (80%), Positives = 412/477 (86%), Gaps = 24/477 (5%) gbl|AAD50296.1|AF173009_1 rep

2925.1 Best-BlastP=> >nrprot 61% Identities = 81/447 (18%), Positives = 193/447 (43%), Gaps = 55/447 (12%) pir|E71606 hypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum) Length = 980

2926.1 Best-BlastP=> >nrprot No Hits found

2928.2 Best-BlastP=> >nrprot 63% Identities = 116/298 (38%), Positives = 178/298 (59%), Gaps = 22/298 (7%) ref|ZP_00031876.1| COG1281: Disulfide bond chaperones of the HSP33 family [Burkholderia fungorum] Length = 316

2929.1 Best-BlastP=> >nrprot 46% Identities = 50/130 (38%), Positives = 77/130 (59%), Gaps = 1/130 (0%) ref|NP_635963.1| conserved hypothetical protein [Xanthomonas campestris campestris pv. campestris str. ATCC 33913] gbl|AAM39887.1| conserved hypothetical protein [Xanthomonas campestris str. ATCC 33913] Length = 171

2932.2 Best-BlastP=> >nrprot 89% Identities = 326/417 (78%), Positives = 374/417 (89%) ref|NP_820428.1| NADH dehydrogenase I, D subunit [Coxiella burnetii RSA 493] gbl|AAO090942.1| NADH dehydrogenase I, D subunit [Coxiella burnetii RSA 493] Length = 417

2932.2 Best-BlastP=> >nrprot 60% Identities = 309/814 (37%), Positives = 491/814 (60%), Gaps = 18/814 (2%) ref|NP_890811.1| probable membrane protein [Bordetella bronchiseptica] emb|CAE34640.1| probable membrane protein [Bordetella bronchiseptica] Length = 1028

2933.2 Best-BlastP=> >nrprot 60% Identities = 122/303 (40%), Positives = 184/303 (60%), Gaps = 14/303 (4%) ref|NP_603145.1| Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gbl|AAL94444.1| Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 310

2934.1 Best-BlastP=> >nrprot No Hits found

2938.3 Best-BlastP=> >nrprot 41% Identities = 250/1286 (19%), Positives = 507/1286 (39%), Gaps = 229/1286 (17%) ref|NP_212646.1| B. burgdorferi predicted coding region BB0512 [Borrelia burgdorferi] pir|G70163 hypothetical protein BB0512 - Lyme disease spirochete gbl|AAC66876.1| B. burgdorferi predicted coding region BB0512 [Borrelia burgdorferi] B31] Length = 2166

2941.1 Best-BlastP=> >nrprot 67% Identities = 121/219 (55%), Positives = 153/219 (69%), Gaps = 1/219 (0%) ref|NP_820429.1| NADH dehydrogenase I, C subunit [Coxiella burnetii RSA 493] gbl|AAO090943.1| NADH dehydrogenase I, C subunit [Coxiella burnetii RSA 493] Length = 227

2941.1 Best-BlastP=> >nrprot 49% Identities = 173/480 (36%), Positives = 267/480 (55%), Gaps = 7/480 (1%) ref|NP_819594.1| apolipoprotein N-acyltransferase [Coxiella burnetii RSA 493] gbl|AAO90108.1| apolipoprotein N-acyltransferase [Coxiella burnetii RSA 493] Length = 485

2942.1 Best-BlastP=> >nrprot 76% Identities = 502/825 (60%), Positives = 628/825 (76%), Gaps = 8/825 (0%) ref|NP_819590.1| leucyl-tRNA synthetase [Coxiella burnetii RSA 493] gbl|AAO90104.1| leucyl-tRNA synthetase [Coxiella burnetii RSA 493] Length = 820

2943.1 Best-BlastP=> >nrprot 42% Identities = 48/160 (30%), Positives = 76/160 (47%), Gaps = 4/160 (2%) ref|NP_252677.1| hypothetical protein [Pseudomonas aeruginosa PA01] ref|ZP_00137430.1| COG2980: Rare lipoprotein B [Pseudomonas aeruginosa UCBPP-PA14] pir|F83148 hypothetical protein PA3988 [imported] - Pseudomonas aeruginosa (strain PAO1) gbl|AGI07375.1|AE004816_11 hypothetical protein PA3988 [Pseudomonas aeruginosa PAO1] Length = 207

2949.2 Best-BlastP=> >nrprot 74% Identities = 185/307 (60%), Positives = 238/307 (77%) ref|ZP_00087322.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 325

295.1 Best-BlastP=> >nrprot 88% Identities = 128/152 (84%), Positives = 141/152 (92%) ref|ZP_000223480.1| COG0377: NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases [Ralstonia metallidurans] Length = 160

2951.2 Best-BlastP=> >nrprot 26% Identities = 100/453 (22%), Positives = 179/453 (39%), Gaps = 86/453 (18%) ref|NP_703829.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD50441.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1321

2952.1 Best-BlastP=> >nrprot 8% Identities = 32/93 (34%), Positives = 53/93 (56%), Gaps = 4/93 (4%) gbl|AAL78307.1|AF288617_4 Dott [Legionella longbeachae] Length = 212

2953.2 Best-BlastP=> >nrprot 97% Identities = 161/166 (96%), Positives = 163/166 (98%) pir|S49042 global stress protein gspA - Legionella pneumophila Length = 166

2954.3 Best-BlastP=> >nrprot 74% Identities = 198/312 (63%), Positives = 247/312 (79%), Gaps = 5/312 (1%) ref|NP_903586.1| probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] gbl|AAQ61577.1| probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 539

2955.2 Best-BlastP=> >nrprot 99% Identities = 126/127 (99%), Positives = 127/127 (100%) gbl|AAD51393.1|AF117715_2 unknown [Legionella pneumophila] Length = 127

2958.2 Best-BlastP=> >nrprot 98% Identities = 248/252 (98%), Positives = 250/252 (99%), Gaps = 1/252 (0%) sp|Q9S4T3|SURE_LEGPN Acid phosphatase surE gb|AAD51394.1|AF117715_3 survival protein homolog [Legionella pneumophila] Length = 251

2959.1 Best-BlastP=> >nrprot 97% Identities = 242/247 (97%), Positives = 243/247 (98%) gb|AAD51395.1|AF117715_4 novel lipoprotein homolog [Legionella pneumophila] Length = 247

296.1 Best-BlastP=> >nrprot 78% Identities = 76/118 (64%), Positives = 93/118 (78%) ref|NP_820431.1| NADH dehydrogenase I, A subunit [Coxiella burnetii RSA 493] gb|AAC90945.1|NADH dehydrogenase I, A subunit [Coxiella burnetii RSA 493] Length = 118

2960.1 Best-BlastP=> >nrprot 99% Identities = 337/341 (98%), Positives = 340/341 (99%) gb|AAD51396.1|AF117715_5 stationary phase specific sigma factor homolog [Legionella pneumophila] Length = 341

2961.1 Best-BlastP=> >nrprot 99% Identities = 410/416 (98%), Positives = 414/416 (99%) sp|Q9S4T0|HGD_LEGPN Homogentisate 1,2-dioxygenase (Homogentisic acid) (Homogentisate oxygenase) (Homogentisic acid oxidase) Length = 416

2962.1 Best-BlastP=> >nrprot 95% Identities = 235/238 (98%), Positives = 236/238 (99%) gb|AAD51398.1|AF117715_7 YebC [Legionella pneumophila] Length = 238

2963.2 Best-BlastP=> >nrprot 59% Identities = 110/257 (42%), Positives = 151/257 (58%), Gaps = 10/257 (3%) ref|NP_231867.1| hydroxyacylglutathione hydrolase GhoB, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir|A82102 probable hydroxyacylglutathione hydrolase GhoB, putative [Vibrio cholerae (strain N16961 serogroup O1) biovar eltor str. N16961] Length = 252

2964.1 Best-BlastP=> >nrprot 62% Identities = 121/275 (44%), Positives = 177/275 (64%), Gaps = 3/275 (1%) ref|NP_229844.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82353 conserved hypothetical protein VC0187 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93363.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 279

2965.1 Best-BlastP=> >nrprot No Hits found

2966.1 Best-BlastP=> >nrprot 73% Identities = 164/276 (59%), Positives = 209/276 (75%), Gaps = 1/276 (0%) ref|NP_438767.1| methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase [Haemophilus influenzae Rd] sp|P44313|FOLD_HAEIN Fold bifunctional protein [Includes: Methylenetetrahydrofolate dehydrogenase ; Methylenetetrahydrofolate cyclohydrolase] pir|A64081 methylenetetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) / methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) - Haemophilus influenzae (strain Rd KW20) gb|AAC22268.1| methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase (fold) [Haemophilus influenzae Rd] Length = 282

2967.1 Best-BlastP=> >nrprot No Hits found

2968.3 Best-BlastP=> >nrprot 13% Identities = 115/119 (96%), Positives = 117/119 (98%) gb|AAM21056.1| FimV [Legionella pneumophila] Length = 119

2969.1 Best-BlastP=> >nrprot 81% Identities = 50/79 (63%), Positives = 64/79 (81%) ref|NP_389755.1| similar to transcriptional regulator [Bacillus subtilis] pir|C69931 transcription regulator homolog yozG - Bacillus subtilis emb|CAB13766.1| yozG [Bacillus subtilis subsp. subtilis str. 168] Length = 84

297.2 Best-BlastP=> >nrprot 63% Identities = 59/101 (58%), Positives = 69/101 (68%), Gaps = 8/101 (7%) ref|NP_820432.1| preprotein translocase, SecG subunit [Coxiella burnetii RSA 493] gb|AAO90946.1| preprotein translocase, SecG subunit [Coxiella burnetii RSA 493] Length = 98

2970.2 Best-BlastP=>>nrprot 32% Identities = 34/103 (33%), Positives = 56/103 (54%) ref|ZP_00136103.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 185

2972.3 Best-BlastP=>>nrprot 10% Identities = 43/138 (31%), Positives = 63/138 (45%), Gaps = 15/138 (10%) ref|NP_704193.1| ubiquitin carboxy-terminal hydrolase, putative [Plasmodium falciparum 3D7] Length = 3183

2973.2 Best-BlastP=>>nrprot No Hits found

2975.2 Best-BlastP=>>nrprot No Hits found

2976.1 Best-BlastP=>>nrprot No Hits found

2978.1 Best-BlastP=>>nrprot 22% Identities = 41/121 (33%), Positives = 64/121 (52%), Gaps = 11/121 (9%) ref|NP_818058.1| gp85 [Mycobacteriophage Che9d] gb|AAN08003.1| gp85 [Mycobacteriophage Che9d] Length = 301

2982.1 Best-BlastP=>>nrprot 38% Identities = 174/388 (44%), Positives = 236/388 (60%), Gaps = 17/388 (4%) ref|NP_706610.1| orf, partial conserved hypothetical protein [Shigella flexneri 2a str. 301] ref|NP_836390.1| putative bacteriophage protein [Shigella flexneri 2a str. 24577]

gb|AAN42317.1|AE015098.7 orf, partial conserved hypothetical protein [Shigella flexneri 2a str. 24577] Length = 619

2983.1 Best-BlastP=>>nrprot 54% Identities = 33/66 (50%), Positives = 47/66 (71%) ref|NP_478090.1| hypothetical protein [Corynebacterium glutamicum] emb|CAD12221.1| hypothetical protein [Corynebacterium glutamicum] Length = 81

2985.1 Best-BlastP=>>nrprot No Hits found

2986.1 Best-BlastP=>>nrprot No Hits found

2987.1 Best-BlastP=>>nrprot No Hits found

2988.1 Best-BlastP=>>nrprot No Hits found

2990.1 Best-BlastP=>>nrprot 44% Identities = 34/97 (35%), Positives = 49/97 (50%), Gaps = 1/97 (1%) ref|NP_771656.1| bli5016 [Bradyrhizobium japonicum] dbj|BAC50281.1| bli5016 [Bradyrhizobium japonicum USDA 110] Length = 198

2991.1 Best-BlastP=>>nrprot 43% Identities = 90/344 (26%), Positives = 145/344 (42%), Gaps = 68/344 (19%) gb|AAC01562.1| S adenosylhomocysteine hydrolase [Thermotoga maritima] Length = 404

2992.2 Best-BlastP=>>nrprot 14% Identities = 38/68 (55%), Positives = 50/68 (73%), Gaps = 1/68 (1%) gb|EAA26507.1| unknown [Rickettsia sibirica] Length = 73

2993.2 Best-BlastP=>>nrprot 31% Identities = 40/160 (25%), Positives = 76/160 (47%), Gaps = 11/160 (6%) dbj|BAA00448.1| open reading frame (196 AA) [Mus musculus] Length = 196

2994.2

Best-BlastP=>>nrprot 65% Identities = 55/118 (46%), Positives = 82/118 (69%) ref|NP_353891.1| AGR_C_1587p [Agrobacterium tumefaciens] ref|NP_531567.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|C97465 hypothetical protein AGR_C_1587 [Imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AE2683 conserved hypothetical protein Atu0869 [Imported] gb|AAL41883.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 122

2995.1 Best-BlastP=>>nrprot 32% Identities = 68/290 (23%), Positives = 135/290 (46%), Gaps = 39/290 (13%) ref|NP_473345.2| hypothetical protein [Plasmodium falciparum 3D7] emb|CAB39052.2| hypothetical protein [Plasmodium falciparum 3D7] Length = 670

2996.1 Best-BlastP=>>nrprot No Hits found

2998.1 Best-BlastP=>>nrprot 51% Identities = 44/134 (32%), Positives = 73/134 (54%), Gaps = 1/134 (0%) ref[NP_820925.1] hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91439.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 148

2999.3 Best-BlastP=>>nrprot 24% Identities = 39/156 (25%), Positives = 69/156 (44%), Gaps = 33/156 (21%) ref[ZP_00047224.1] COG3774: Mannosyltransferase OCH1 and related enzymes Length = 233

3.1 Best-BlastP=>>nrprot 49% Identities = 36/79 (45%), Positives = 50/79 (63%) ref[NP_907749.1] hypothetical protein WS1616 [Wolinella succinogenes] emb|CAE10649.1| hypothetical protein [Wolinella succinogenes] Length = 96

30.1 Best-BlastP=>>nrprot No Hits found

300.2 Best-BlastP=>>nrprot 75% Identities = 346/570 (60%), Positives = 431/570 (75%), Gaps = 3/570 (0%) ref[NP_752183.1] Poly-tRNA synthetase [Escherichia coli CFT073] gb|AAN78727.1|AE016755_227 Poly-tRNA synthetase [Escherichia coli CFT073] Length = 590

3000.1 Best-BlastP=>>nrprot 58% Identities = 312/711 (43%), Positives = 440/711 (61%), Gaps = 35/711 (4%) ref[ZP_00090403.1] COG3243: Poly(3-hydroxyalkanoate) synthetase [Azotobacter vinelandii] Length = 824

3001.1 Best-BlastP=>>nrprot No Hits found

3002.1 Best-BlastP=>>nrprot 36% Identities = 96/343 (27%), Positives = 152/343 (44%), Gaps = 29/343 (8%) ref[ZP_00019713.1] hypothetical protein [Chloroflexus aurantiacus] Length = 360

3003.1 Best-BlastP=>>nrprot 57% Identities = 77/202 (38%), Positives = 119/202 (58%), Gaps = 3/202 (1%) ref[ZP_00008122.1] COG0500: SAM-dependent methyltransferases [Rhodobacter sphaeroides] Length = 204

3005.2 Best-BlastP=>>nrprot 69% Identities = 74/164 (45%), Positives = 116/164 (70%), Gaps = 2/164 (1%) ref[NP_924145.1] hypothetical protein gll|1199 [Gloeoobacter violaceus] dbj|BAC89140.1|gll|1199 [Gloeoobacter violaceus] Length = 175

3008.1 Best-BlastP=>>nrprot 55% Identities = 65/195 (33%), Positives = 114/195 (58%), Gaps = 1/195 (0%) ref[NP_820992.1] conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91506.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 203

3009.2 Best-BlastP=>>nrprot No Hits found

3011.2 Best-BlastP=>>nrprot 49% Identities = 88/315 (27%), Positives = 164/315 (52%), Gaps = 27/315 (8%) ref[NP_819925.1] hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90439.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 324

3013.2 Best-BlastP=>>nrprot 48% Identities = 48/152 (31%), Positives = 75/152 (49%), Gaps = 5/152 (3%) ref[NP_720010.1] acetyltransferase, GNAT family [Shewanella oneidensis MR-1] gb|AAN57454.1|AE015881_1 acetyltransferase, GNAT family [Shewanella oneidensis MR-1] Length = 154

3014.1 Best-BlastP=>>nrprot 48% Identities = 57/192 (29%), Positives = 98/192 (51%), Gaps = 22/192 (11%) ref[NP_656418.1] APS kinase, Adenylylsulfate kinase [Bacillus anthracis A2012] ref[NP_844924.1] hypothetical protein [Bacillus anthracis str. Ames] gb|AAP26410.1| hypothetical protein BA2556 [Bacillus anthracis str. Ames] Length = 186

3015.1 Best-BlastP=>>nrprot 50% Identities = 83/250 (33%), Positives = 124/250 (49%), Gaps = 7/250 (2%) ref[NP_656739.1] Ubie_methyltran, ubiE|COQ5 methyltransferase family [Bacillus anthracis A2012] ref[NP_845200.1] conserved hypothetical protein [Bacillus anthracis str. Ames] gb|AAP26686.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 254

3016.1 Best-BlastP=>>nrprot No Hits found

3017.1 Best-BlastP=>>nrprot No Hits found

3018.1 Best-BlastP=>>nrprot No Hits found

3022.1 Best-BlastP=>>nrprot No Hits found

3023.1 Best-BlastP=>>nrprot 58% Identities = 26/56 (46%), Positives = 41/56 (73%) ref|NP_832415.1| Glutamate-rich protein grpB [Bacillus cereus ATCC 14579] gbl|AAP09616.1| Glutamate-rich protein grpB [Bacillus cereus ATCC 14579] Length = 168

3024.1 Best-BlastP=>>nrprot 76% Identities = 253/425 (59%), Positives = 326/425 (76%), Gaps = 2/425 (0%) ref|ZP_00091804.1| COG0172: Seryl-tRNA synthetase [Azotobacter vinelandii] Length = 607

3027.1 Best-BlastP=>>nrprot 68% Identities = 86/149 (57%), Positives = 111/149 (74%) gbl|AAM89273.1|AF528189_2 SecB [Serratia marcescens] Length = 156

3028.1 Best-BlastP=>>nrprot 75% Identities = 48/83 (57%), Positives = 64/83 (77%) ref|ZP_00089760.1| COG0695: Glutaredoxin and related proteins [Azotobacter vinelandii] Length = 84

3030.2 Best-BlastP=>>nrprot 63% Identities = 70/163 (42%), Positives = 104/163 (63%), Gaps = 2/163 (1%) ref|ZP_00021668.1| COG2606: Uncharacterized conserved protein [Raistonia metalidurans] Length = 165

3031.2 Best-BlastP=>>nrprot 42% Identities = 37/136 (27%), Positives = 60/136 (44%), Gaps = 2/136 (1%) ref|NP_347707.1| Hypothetical protein [Clostridium acetobutylicum] pirl|D97032 hypothetical protein CAC1073 [imported] - Clostridium acetobutylicum gbl|AAK79047.1|AE007622_9 Hypothetical protein [Clostridium acetobutylicum] Length = 152

3035.2 Best-BlastP=>>nrprot 62% Identities = 89/185 (48%), Positives = 120/185 (64%), Gaps = 9/185 (4%) ref|NP_753759.1| Hypothetical protein ydcN [Escherichia coli CFT073] gbl|AAN80321.1|AE016760_180 Hypothetical protein ydcN [Escherichia coli CFT073] Length = 178

3036.2 Best-BlastP=>>nrprot 46% Identities = 54/146 (36%), Positives = 85/146 (58%), Gaps = 5/146 (3%) ref|NP_349095.1| Predicted kinase from adenilate kinase family, FLAR-like protein [Clostridium acetobutylicum] pirl|H97205 probable kinase from adenilate kinase family, FLAR-like protein [imported] - Clostridium acetobutylicum gbl|AAK80435.1|AE007747_4 Predicted kinase from adenilate kinase family, FLAR-like protein [Clostridium acetobutylicum] Length = 177

304.2 Best-BlastP=>>nrprot 21% Identities = 122/500 (24%), Positives = 202/500 (40%), Gaps = 87/500 (17%) gbl|AAH16985.2| Unknown (protein for MGC:21968) [Homo sapiens] Length = 579

3041.1 Best-BlastP=>>nrprot 16% Identities = 33/146 (22%), Positives = 67/146 (45%), Gaps = 20/146 (13%) gbl|AAQ55479.1| hypothetical protein [Methanococcus voltae] Length = 178

3042.1 Best-BlastP=>>nrprot No Hits found

3045.3 Best-BlastP=>>nrprot 58% Identities = 162/484 (33%), Positives = 261/484 (53%), Gaps = 46/484 (9%) gbl|AAP68896.1| putative N5-nucleotidase [Oryza sativa (japonica cultivar-group)] Length = 569

3046.3 Best-BlastP=>>nrprot 26% Identities = 39/103 (37%), Positives = 50/103 (48%), Gaps = 10/103 (9%) pirl|F72654 hypothetical protein APE0666-Aeropyrum pernix (strain K1) dbl|BA79638.1|102aa long hypothetical protein [Aeropyrum pernix] Length = 102

3047.2 Best-BlastP=>>nrprot 73% Identities = 131/210 (62%), Positives = 159/210 (75%) ref|NP_716775.1| ribose 5-phosphate isomerase [Shewanella oneidensis MR-1] sp|Q8EHR7|RPIA_SHEON Ribose 5-phosphate isomerase A (Phosphoriboisomerase A) (PRI) gbl|AAN54220.1|AE015559_4 ribose 5-phosphate isomerase [Shewanella oneidensis MR-1] Length = 219

3049.1 Best-BlastP=>>nrprot 69% Identities = 133/239 (55%), Positives = 174/239 (72%), Gaps = 1/239 (0%) ref|NP_746983.1| RNA methyltransferase, TrmH family, group 3 [Pseudomonas putida KT2440] gb|AAN70447.1|AE016686_1 RNA methyltransferase, TrmH family, group 3 [Pseudomonas putida KT2440] Length = 248

3052.2 Best-BlastP=>>nrprot 69% Identities = 124/236 (52%), Positives = 167/236 (70%) ref|NP_820118.1| dienelactone hydrolase family protein [Coxiella burnetii RSA 493] gb|AAO90632.1| dienelactone hydrolase family protein [Coxiella burnetii RSA 493] Length = 237

3053.3 Best-BlastP=>>nrprot 54% Identities = 40/122 (32%), Positives = 80/122 (65%), Gaps = 4/122 (3%) gb|AAA29909.1| ORF 3 Length = 393

3054.3 Best-BlastP=>>nrprot 59% Identities = 117/304 (38%), Positives = 170/304 (55%), Gaps = 27/304 (8%) ref|ZP_00067579.1| COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Microbulbifer degradans 2-40] Length = 658

3055.1 Best-BlastP=>>nrprot 52% Identities = 114/330 (34%), Positives = 164/330 (49%), Gaps = 35/330 (10%) ref|NP_718657.1| TPR domain protein [Shewanella oneidensis MR-1] gb|AAN56101.1|AE015746_5 TPR domain protein [Shewanella oneidensis MR-1] Length = 679

3057.1 Best-BlastP=>>nrprot 61% Identities = 150/319 (47%), Positives = 213/319 (66%), Gaps = 9/319 (2%) ref|ZP_00087368.1| COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Pseudomonas fluorescens PRO-1] Length = 359

3058.1 Best-BlastP=>>nrprot No Hits found

3059.2 Best-BlastP=>>nrprot 99% Identities = 258/259 (99%), Positives = 259/259 (100%) emb|CAA066664.1| 29 kDa immunogenic protein [Legionella pneumophila] Length = 259

306.1 Best-BlastP=>>nrprot 75% Identities = 290/467 (62%), Positives = 356/467 (76%), Gaps = 1/467 (0%) ref|NP_254123.1| probable biotin carboxylase subunit of a transcarboxylase [Pseudomonas aeruginosa PA01] pir|G82966 probable biotin carboxylase subunit of a transcarboxylase PA5436 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG08821.1|AE004956_5 probable biotin carboxylase subunit of a transcarboxylase [Pseudomonas aeruginosa PA01] Length = 471

3060.1 Best-BlastP=>>nrprot No Hits found

3061.2 Best-BlastP=>>nrprot 72% Identities = 119/204 (58%), Positives = 156/204 (76%), Gaps = 2/204 (0%) ref|ZP_00084510.1| COG2011: ABC-type metal ion transport system, permease component [Pseudomonas fluorescens PfO-1] Length = 224

3063.2 Best-BlastP=>>nrprot 69% Identities = 174/343 (50%), Positives = 238/343 (69%), Gaps = 7/343 (2%) ref|NP_873575.1| D-methionine transport ATP-binding protein MetN [Haemophilus ducreyi 35000HP] gb|AAP95964.1| D-methionine transport ATP-binding protein MetN [Haemophilus ducreyi 35000HP] Length = 344

3065.1 Best-BlastP=>>nrprot 40% Identities = 39/138 (28%), Positives = 63/138 (45%), Gaps = 15/138 (10%) ref|NP_520406.1| PUTATIVE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] emb|CAD15992.1| PUTATIVE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] Length = 143

3067.1 Best-BlastP=>>nrprot 54% Identities = 27/100 (27%), Positives = 59/100 (59%), Gaps = 6/100 (6%) ref|NP_820531.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91045.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 124

3068.1 Best-BlastP=>>nrprot 84% Identities = 290/388 (74%), Positives = 331/388 (85%) ref|NP_800128.1| putative acyl-CoA dehydrogenase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61961.1| putative acyl-CoA dehydrogenase [Vibrio parahaemolyticus] Length = 389

3069.1 Best-BlastP=>>nrprot 55% Identities = 83/222 (37%), Positives = 126/222 (56%), Gaps = 4/222 (1%) ref|NP_819980.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90494.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 230

307.2 Best-BlastP=>>nrprot 47% Identities = 54/168 (32%), Positives = 84/168 (50%), Gaps = 8/168 (4%) ref|NP_796502.1| conserved hypothetical protein VP0123 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC58386.1| hypothetical protein [Vibrio parahaemolyticus] Length = 180

3070.2 Best-BlastP=>>nrprot No Hits found

3072.2 Best-BlastP=>>nrprot 67% Identities = 300/598 (50%), Positives = 400/598 (66%), Gaps = 9/598 (1%) ref|NP_637990.1| ATP-dependent RNA helicase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM41914.1| ATP-dependent RNA helicase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 642

3074.1 Best-BlastP=>>nrprot No Hits found

3075.2 Best-BlastP=>>nrprot No Hits found

3077.1 Best-BlastP=>>nrprot 42% Identities = 66/214 (30%), Positives = 103/214 (48%), Gaps = 18/214 (8%) ref|NP_355106.1| AGR_C_3887p [Agrobacterium tumefaciens] ref|NP_532818.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AH2839 conserved hypothetical protein Atu2144 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir|B97617 similar to orf3 gene in methylobacterium extorquens [imported] - Agrobacterium tumefaciens (strain C58, Cereon) gb|AAK87891.1| AGR_C_3887p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL43134.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 257

3078.2 Best-BlastP=>>nrprot 53% Identities = 128/399 (32%), Positives = 219/399 (54%), Gaps = 38/399 (9%) ref|NP_071132.1| hypothetical protein [Archaeoglobus fulgidus DSM 4304] sp|O27977|YN07_ARCFU Hypothetical protein AF2307 pir|C69538 hypothetical protein AF2307 - Archaeoglobus fulgidus gb|AAB88957.1| A. fulgidus predicted coding region AF2307 [Archaeoglobus fulgidus] DSM 4304] Length = 365

3080.2 Best-BlastP=>>nrprot 64% Identities = 210/490 (42%), Positives = 312/490 (63%), Gaps = 12/490 (2%) ref|ZP_00139612.1| COG0189: Glutathione synthase/Ribosomal protein S6 modification enzyme (glutamyl transferase) [Pseudomonas aeruginosa UCBPP-PA14]

3081.2 Best-BlastP=>>nrprot No Hits found

3082.1 Best-BlastP=>>nrprot 67% Identities = 75/157 (47%), Positives = 106/157 (67%) ref|NP_231147.1| hypothetical protein VC1506 [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82191 hypothetical protein VC1506 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94661.1| hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 158

3083.1 Best-BlastP=>>nrprot 48% Identities = 52/171 (30%), Positives = 90/171 (52%), Gaps = 1/171 (0%) ref|NP_404077.1| osmotically inducible protein Y [Yersinia pestis] ref|NP_671042.1| hyperosmotically inducible periplasmic protein [Yersinia pestis KIM] pir|AF0053 osmotically inducible protein Y [imported] - *Yersinia pestis* (strain CO92) emb|CAC89289.1| osmotically inducible protein Y [Yersinia pestis CO92] gb|AM87293.1|AE013978_5 hyperosmotically inducible periplasmic protein [Yersinia pestis KIM] Length = 204

3085.2 Best-BlastP=>>nrprot 84% Identities = 693/944 (73%), Positives = 805/944 (85%), Gaps = 4/944 (0%) ref|NP_819318.1| excinuclease ABC, A subunit [Coxiella burnetii RSA 493] gb|AAO89832.1| excinuclease ABC, A subunit [Coxiella burnetii RSA 493] Length = 954

3086.1 Best-BlastP=>>nrprot 78% Identities = 133/191 (69%), Positives = 152/191 (79%) ref|NP_819577.1| lemA protein [Coxiella burnetii RSA 493] gb|AAO90091.1| lemA protein [Coxiella burnetii RSA 493] Length = 192

3087.1 Best-BlastP=>>nrprot 77% Identities = 198/344 (57%), Positives = 265/344 (77%), Gaps = 6/344 (1%) ref|NP_819578.1| heat shock protein HtpX [Coxiella burnetii RSA 493] gb|AAO90092.1| heat shock protein HtpX [Coxiella burnetii RSA 493] Length = 348

3088.1 Best-BlastP=>>nrprot 71% Identities = 141/251 (56%), Positives = 185/251 (73%) ref|ZP_00128291.1| COG0842: ABC-type multidrug transport system, permease component [Pseudomonas syringae pv. syringae B728a] Length = 262

309.2 Best-BlastP=>>nrprot 67% Identities = 545/1113 (48%), Positives = 752/1113 (67%), Gaps = 2/1113 (0%) ref|NP_820221.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90735.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 1619

3091.1 Best-BlastP=>>nrprot No Hits found

3093.1 Best-BlastP=>>nrprot 73% Identities = 139/243 (57%), Positives = 185/243 (76%), Gaps = 2/243 (0%) ref|NP_928570.1| tRNA (guanine-N1)-methyltransferase (M1G-methyltransferase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13553.1| tRNA (guanine-N1)-methyltransferase (M1G-methyltransferase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 250

3095.1 Best-BlastP=>>nrprot 61% Identities = 65/169 (38%), Positives = 105/169 (62%), Gaps = 7/169 (4%) ref|NP_716978.1| 16S rRNA processing protein RimM [Shewanella oneidensis MR-1] gb|AAN54423.1|AE015579_12| 16S rRNA processing protein RimM [Shewanella oneidensis MR-1] Length = 177

3096.1 Best-BlastP=>>nrprot 74% Identities = 51/85 (60%), Positives = 65/85 (76%) ref|NP_841705.1| Ribosomal protein S16 [Nitrosomonas europaea ATCC 19718] emb|CAD85582.1| Ribosomal protein S16 [Nitrosomonas europaea ATCC 19718] Length = 89

3097.3 Best-BlastP=>>nrprot 79% Identities = 299/447 (66%), Positives = 365/447 (81%), Gaps = 1/447 (0%) ref|NP_716976.1| signal recognition particle protein Ffh [Shewanella oneidensis MR-1] gb|AAN54421.1|AE015579_10| signal recognition particle protein Ffh [Shewanella oneidensis MR-1] Length = 457

310.1 Best-BlastP=>>nrprot No Hits found

3101.1 Best-BlastP=>>nrprot 12% Identities = 46/178 (25%), Positives = 78/178 (43%), Gaps = 12/178 (6%) ref|AAQ73211.1| M protein [Streptococcus pyogenes] Length = 243

3102.2 Best-BlastP=>>nrprot 50% Identities = 61/141 (43%), Positives = 80/141 (56%), Gaps = 3/141 (2%) ref|ZP_00084504.1| COG0735: Fe2+/Zn2+ uptake regulation proteins [Pseudomonas fluorescens PRO-1] Length = 160

3104.2 Best-BlastP=>>nrprot 38% Identities = 208/652 (31%), Positives = 329/652 (50%), Gaps = 68/652 (10%) ref|NP_717300.1| cation transport ATPase, E1-E2 family [Shewanella oneidensis MR-1] gb|AAN54744.1|AE015614_11 cation transport ATPase, E1-E2 family [Shewanella oneidensis MR-1] Length = 753

3105.2 Best-BlastP=>>nrprot 41% Identities = 26/69 (37%), Positives = 42/69 (60%) ref|ZP_00117353.1| COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] Length = 856

3106.2 Best-BlastP=>>nrprot 36% Identities = 149/353 (42%), Positives = 220/353 (62%), Gaps = 3/353 (0%) ref|NP_442598.1| PleD gene product homologue [Synechocystis sp. PCC 6803] pir|S76977 pleD-4 protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10669.1| sfr0302 [Synechocystis sp. PCC 6803] Length = 768

3107.2 Best-BlastP=>>nrprot No Hits found

3109.2 Best-BlastP=>>nrprot 55% Identities = 39/100 (39%), Positives = 63/100 (63%), Gaps = 1/100 (1%) ref|NP_455037.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_459436.1| cytochrome o ubiquinol oxidase subunit IV [Salmonella typhimurium LT2] ref|NP_806150.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi] (strain CT18) pir|AC0557 cytochrome o ubiquinol oxidase C chain [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAL19395.1| cytochrome o ubiquinol oxidase subunit IV [Salmonella typhimurium LT2] embl|CAD08899.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO70010.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 109

3110.1 Best-BlastP=>>nrprot 76% Identities = 128/188 (68%), Positives = 153/188 (81%) ref|NP_820040.1| cytochrome o ubiquinol oxidase, subunit III [Coxiella burnetii RSA 493] gb|AAO90554.1| cytochrome o ubiquinol oxidase, subunit III [Coxiella burnetii RSA 493] Length = 198

3113.1 Best-BlastP=>>nrprot 85% Identities = 482/665 (72%), Positives = 568/665 (85%), Gaps = 3/665 (0%) ref|NP_820041.1| cytochrome o ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] gb|AAO90555.1| cytochrome o ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] Length = 668

3114.2 Best-BlastP=>>nrprot 69% Identities = 173/292 (59%), Positives = 222/292 (76%), Gaps = 10/292 (3%) ref|NP_820042.1| cytochrome o ubiquinol oxidase, subunit II [Coxiella burnetii RSA 493] gb|AAO90556.1| cytochrome o ubiquinol oxidase, subunit II [Coxiella burnetii RSA 493] Length = 298

3116.2 Best-BlastP=>>nrprot 80% Identities = 82/130 (63%), Positives = 106/130 (81%) ref|NP_820044.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90558.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 133

3117.2 Best-BlastP=>>nrprot 68% Identities = 116/211 (54%), Positives = 152/211 (72%), Gaps = 2/211 (0%) ref|ZP_00085665.1| COG0323: DNA mismatch repair enzyme (predicted ATPase) [Pseudomonas fluorescens PfO-1] Length = 262

3118.1 Best-BlastP=>>nrprot No Hits found

3119.1 Best-BlastP=>>nrprot 61% Identities = 111/264 (42%), Positives = 162/264 (61%), Gaps = 7/264 (2%) ref|NP_794780.1| pyrroline-5-carboxylate reductase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58475.1| pyrroline-5-carboxylate reductase [Pseudomonas syringae pv. tomato str. DC3000] Length = 272

312.3 Best-BlastP=>>nrprot No Hits found

3121.2 Best-BlastP=> >nrprot 67% Identities = 119/225 (52%), Positives = 156/225 (69%) ref|ZP_00088980.1| COG0325: Predicted enzyme with a TIM-barrel fold [Azotobacter vinelandii] Length = 234

3124.2 Best-BlastP=> >nrprot 88% Identities = 258/345 (74%), Positives = 305/345 (88%) ref|NP_638103.1| twitching motility protein [Xanthomonas campestris pv. campestris str. ATCC 33913] ref|NP_643233.1| twitching motility protein [Xanthomonas axonopodis pv. citri str. gb|AM37769.1| twitching motility protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM42027.1| twitching motility protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 345

3127.1 Best-BlastP=> >nrprot 99% Identities = 235/235 (100%) sp|Q9X528|RNPH_LEGPN Ribonuclease PH (RNase PH) (tRNA nucleotidyltransferase) gb|ADD282|18.1|AF120720_1 ribonuclease PH [Legionella pneumophila] Length = 235

3128.1 Best-BlastP=> >nrprot 57% Identities = 62/172 (36%), Positives = 95/172 (55%), Gaps = 13/172 (7%) ref|NP_747016.1| conserved hypothetical protein [Pseudomonas putida KT2440] gb|AAN70480.1|AE016689_8 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 172

3129.2 Best-BlastP=> >nrprot 73% Identities = 195/336 (58%), Positives = 247/336 (73%) ref|NP_252513.1| S-adenosylmethionine:tRNA ribosyltransferase isomerase [Pseudomonas aeruginosa PA01] sp|Q9HXH8|QUEA_PSEAE S-adenosylmethionine:tRNA ribosyltransferase (EC 5.4.99.-) queA PA3824 [similarity] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07211.1|AE004799_17 S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Pseudomonas aeruginosa PAO1] Length = 347

3130.1 Best-BlastP=> >nrprot 18% Identities = 31/100 (31%), Positives = 52/100 (52%), Gaps = 3/100 (3%) ref|NP_562861.1| queuine tRNA-ribosyltransferase [Clostridium perfringens] sp|Q8XJ16|TGT_CLOPE Queuine tRNA-ribosyltransferase (tRNA-guanine transglycosylase) (Guanine insertion enzyme) dbj|BAB81651.1| queuine tRNA-ribosyltransferase [Clostridium perfringens str. 13] Length = 380

3131.1 Best-BlastP=> >nrprot 68% Identities = 53/111 (47%), Positives = 77/111 (69%) ref|ZP_00087740.1| COG1862: Preprotein translocase subunit YajC [Pseudomonas fluorescens PfO-1] Length = 111

3132.1 Best-BlastP=> >nrprot No Hits found

3133.2 Best-BlastP=> >nrprot No Hits found

3134.1 Best-BlastP=> >nrprot 57% Identities = 65/150 (43%), Positives = 91/150 (60%), Gaps = 6/150 (4%) ref|NP_419685.1| hypothetical protein [Caulobacter crescentus CB15] pir|A87357 hypothetical protein CC0868 [imported] - Caulobacter crescentus gb|AAK22853.1| hypothetical protein [Caulobacter crescentus CB15] Length = 196

3135.1 Best-BlastP=> >nrprot 69% Identities = 43/63 (68%), Positives = 49/63 (77%) ref|ZP_00067639.1| COG4728: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] Length = 93

3136.1 Best-BlastP=> >nrprot 54% Identities = 38/105 (36%), Positives = 60/105 (57%), Gaps = 2/105 (1%) gb|AAN62313.1|AF440524_100 conserved hypothetical protein [Pseudomonas aeruginosa] Length = 130

3137.1 Best-BlastP=> >nrprot No Hits found

3138.2 Best-BlastP=> >nrprot No Hits found

3142.2 Best-BlastP=> >nrprot 53% Identities = 106/281 (37%), Positives = 158/281 (56%), Gaps = 19/281 (6%) ref|ZP_00065061.1| COG3951: Rod binding protein [Microbulbifer degradans 2-40] Length = 318

3145.1 Best-BlastP=> >nrprot No Hits found

3146.2 Best-BlastP=> >nrprot 48% Identities = 74/241 (30%), Positives = 122/241 (50%), Gaps = 7/241 (2%) ref|NP_928923.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] Length = 279

3147.1 Best-BlastP=> >nrprot 78% Identities = 107/158 (67%), Positives = 127/158 (80%) ref|NP_439483.1| transcription elongation factor [Haemophilus influenzae Rd] sp|P43881|GRE_A_HAEIN Transcription elongation factor greA (Transcript cleavage factor greA) pirl|B64117 transcription elongation factor greA - Haemophilus influenzae (strain Rd KW20) gb|AAC22976.1| transcription elongation factor (greA) [Haemophilus influenzae Rd] Length = 158

3148.1 Best-BlastP=> >nrprot 55% Identities = 101/297 (34%), Positives = 150/297 (50%), Gaps = 36/297 (12%) ref|NP_842462.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD86383.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 304

3149.1 Best-BlastP=> >nrprot 36% Identities = 69/341 (20%), Positives = 132/341 (38%), Gaps = 53/341 (15%) ref|NP_616447.1| hypothetical protein (multi-domain) [Methanoscarcina acetivorans str. C2A] gb|AAM04927.1| hypothetical protein (multi-domain) [Methanoscarcina acetivorans str. C2A] Length = 584

315.3 Best-BlastP=> >nrprot 37% Identities = 97/212 (45%), Positives = 127/212 (59%) gb|AO50865.1| similar to Leishmania major. Ppg3 [Dictyostelium discoideum] Length = 374

3150.1 Best-BlastP=> >nrprot 60% Identities = 94/212 (44%), Positives = 138/212 (65%), Gaps = 3/212 (1%) ref|NP_819377.1| acid phosphatase, class B [Coxiella burnetii RSA 493] gb|AO89891.1| acid phosphatase, class B [Coxiella burnetii RSA 493] Length = 221

3152.1 Best-BlastP=> >nrprot 98% Identities = 174/177 (98%), Positives = 176/177 (99%) gb|AAM0398.1|AF386079_8 CcmG [Legionella pneumophila] Length = 177

3153.3 Best-BlastP=> >nrprot 99% Identities = 643/650 (98%), Positives = 649/650 (99%) gb|AAM0397.1|AF386079_7 CcmF [Legionella pneumophila] Length = 650

3157.1 Best-BlastP=> >nrprot 98% Identities = 142/143 (99%), Positives = 142/143 (99%) gb|AAM0396.1|AF386079_6 CcmE [Legionella pneumophila] Length = 143

3158.1 Best-BlastP=> >nrprot 97% Identities = 72/73 (98%), Positives = 72/73 (98%) gb|AAM00395.1|AF386079_5 CcmD [Legionella pneumophila] Length = 73

3159.2 Best-BlastP=> >nrprot 98% Identities = 247/251 (98%), Positives = 249/251 (99%) gb|AAM00394.1|AF386079_4 CcmC [Legionella pneumophila] Length = 251

3160.1 Best-BlastP=> >nrprot No Hits found

3161.1 Best-BlastP=> >nrprot 44% Identities = 60/224 (26%), Positives = 103/224 (45%), Gaps = 13/224 (5%) gb|AAK18828.1|AF327739_5 Peb1 [Streptococcus thermophilus] Length = 277

3163.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614_2 unknown [Francisella tularensis subsp. tularensis] Length = 94

3165.1 Best-BlastP=> >nrprot No Hits found

3166.1 Best-BlastP=> >nrprot 65% Identities = 99/176 (56%), Positives = 127/176 (72%), Gaps = 2/176 (1%) ref|NP_903124.1| probable DNA-directed DNA polymerase, bacteriophage-type [Chromobacterium violaceum ATCC 12472] gb|AAQ61115.1| probable DNA-directed DNA polymerase, bacteriophage-type [Chromobacterium violaceum ATCC 12472] Length = 280

3167.1 Best-BlastP=> >nrprot 63% Identities = 199/415 (47%), Positives = 270/415 (65%), Gaps = 4/415 (0%) ref|NP_820906.1| transporter, putative [Coxiella burnetii RSA 493] gb|AAO91420.1| transporter, putative [Coxiella burnetii RSA 493] Length = 435

3169.1 Best-BlastP=> >nrprot 50% Identities = 90/186 (48%), Positives = 122/186 (65%), Gaps = 3/186 (1%) ref|NP_926264.1| unknown protein [Gloeobacter violaceus] dbj|BAC91259.1| glr3318 [Gloeobacter violaceus] Length = 228

317.1 Best-BlastP=> >nrprot 59% Identities = 142/362 (39%), Positives = 202/362 (55%), Gaps = 33/362 (9%) ref|ZP_00069313.1| COG0517: FOG: CBS domain [Oenococcus oeni MCV] Length = 382

3172.2 Best-BlastP=> >nrprot 68% Identities = 118/270 (43%), Positives = 188/270 (69%), Gaps = 5/270 (1%) ref|ZP_00014387.1| COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Rhodospirillum rubrum] Length = 369

3173.1 Best-BlastP=> >nrprot 63% Identities = 38/88 (43%), Positives = 54/88 (61%), Gaps = 3/88 (3%) ref|ZP_00068002.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 128

3174.1 Best-BlastP=> >nrprot 53% Identities = 100/270 (37%), Positives = 155/270 (57%), Gaps = 1/270 (0%) ref|NP_903183.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61174.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 276

3175.1 Best-BlastP=> >nrprot 35% Identities = 51/201 (25%), Positives = 92/201 (45%), Gaps = 3/201 (1%) ref|NP_903184.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61175.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 255

3177.1 Best-BlastP=> >nrprot 54% Identities = 64/138 (46%), Positives = 84/138 (60%), Gaps = 14/138 (10%) ref|NP_903185.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61176.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 145

3178.1 Best-BlastP=> >nrprot 72% Identities = 124/219 (56%), Positives = 157/219 (71%), Gaps = 4/219 (1%) ref|ZP_00066950.1| COG0036: Pentose-5-phosphate-3-epimerase [Microbulbifer degradans 2-40] Length = 228

3179.1 Best-BlastP=> >nrprot 47% Identities = 179/574 (31%), Positives = 288/574 (50%), Gaps = 25/574 (4%) ref|ZP_00067610.1| COG0741: Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) [Microbulbifer degradans 2-40] Length = 669

318.2 Best-BlastP=> >nrprot 76% Identities = 266/465 (57%), Positives = 361/465 (77%), Gaps = 7/465 (1%) ref|NP_902486.1| probable PhoH-related protein [Chromobacterium violaceum ATCC 12472] gb|AAQ60484.1| probable PhoH-related protein [Chromobacterium violaceum ATCC 12472] Length = 467

3181.2 Best-BlastP=> >nrprot 66% Identities = 154/327 (47%), Positives = 218/327 (66%) ref|ZP_00016063.1| COG0842: ABC-type multidrug transport system, permease component [Rhodospirillum rubrum] Length = 371

3184.3 Best-BlastP=> >nrprot 71% Identities = 221/407 (54%), Positives = 299/407 (73%), Gaps = 7/407 (1%) ref|NP_820219.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90733.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 445

3186.2 Best-BlastP=>>nrprot 71% Identities = 622/1145 (54%), Positives = 830/1145 (72%), Gaps = 9/1145 (0%) ref|NP_791924.1| transcription-repair coupling factor [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO55619.1| transcription-repair coupling factor [Pseudomonas syringae pv. tomato str. DC3000] Length = 1150

3190.1 Best-BlastP=>>nrprot 42% Identities = 89/233 (38%), Positives = 127/233 (54%), Gaps = 2/233 (0%) ref|NP_519922.1| GALA PROTEIN 3 [Ralstonia solanacearum] Length = 522

3191.1 Best-BlastP=>>nrprot No Hits found

3193.2 Best-BlastP=>>nrprot 50% Identities = 77/223 (34%), Positives = 116/223 (52%), Gaps = 7/223 (3%) spl|P57974|RECO_PASMU DNA repair protein recO (Recombination protein O) Length = 240

3196.3 Best-BlastP=>>nrprot 65% Identities = 225/478 (47%), Positives = 330/478 (69%), Gaps = 2/478 (0%) ref|NP_462493.1| putative POT family, peptide transport protein [Salmonella typhimurium LT2] gb|AAL22452.1| putative POT family peptide transport protein [Salmonella typhimurium LT2] Length = 489

3198.1 Best-BlastP=>>nrprot 54% Identities = 72/174 (41%), Positives = 101/174 (58%), Gaps = 1/174 (0%) ref|ZP_00081025.1| COG0558: Phosphatidylglycerophosphate synthase [Geobacter metallireducens] Length = 198

3199.1 Best-BlastP=>>nrprot 98% Identities = 561/575 (97%), Positives = 566/575 (98%) gb|AAC44717.1| FrgA [Legionella pneumophila] Length = 575

3201.1 Best-BlastP=>>nrprot 81% Identities = 451/609 (74%), Positives = 520/609 (85%), Gaps = 3/609 (0%) ref|NP_820341.1| ATP-dependent metalloprotease FtsH [Coxiella burnetii RSA 493] Length = 647

3205.3 Best-BlastP=>>nrprot 46% Identities = 466/1207 (38%), Positives = 682/1207 (56%), Gaps = 45/1207 (3%) emb|CAC01603.1| peptide synthetase [Anabaena sp. 90] Length = 2258

3207.5 Best-BlastP=>>nrprot 50% Identities = 247/840 (29%), Positives = 419/840 (49%), Gaps = 91/840 (10%) ref|NP_819809.1| sensory box histidine kinase/response regulator [Coxiella burnetii RSA 493] gb|AAO90323.1| sensory box histidine kinase/response regulator [Coxiella burnetii RSA 493] Length = 808

321.3 Best-BlastP=>>nrprot 22% Identities = 44/165 (26%), Positives = 67/165 (40%), Gaps = 22/165 (13%) pir|T18253| probable mitochondrial carrier protein - yeast [Candida albicans] emb|CAA22027.1| putative mitochondrial carrier protein [Candida albicans] Length = 284

3212.2 Best-BlastP=>>nrprot 45% Identities = 64/206 (31%), Positives = 105/206 (50%), Gaps = 11/206 (5%) ref|NP_389092.1| similar to endo-1,4-beta-xylanase [Bacillus subtilis] spl|C34798|YJEA_BACSU Hypothetical protein yjeA precursor pir|G69849| endo-1,4-beta-xylanase homolog yjeA Bacillus subtilis gb|AAC46306.1| NodB-like protein [Bacillus subtilis] emb|CAB13067.1| yjeA [Bacillus subtilis subsp. subtilis str. 168] = 467

3217.3 Best-BlastP=>>nrprot 79% Identities = 261/396 (65%), Positives = 314/396 (79%), Gaps = 3/396 (0%) ref|NP_819161.1| 2-amino-3-ketobutyrate coenzyme A ligase [Coxiella burnetii RSA 493] Length = 396

3218.1 Best-BlastP=>>nrprot 59% Identities = 94/211 (44%), Positives = 129/211 (61%) ref|NP_840138.1| possible pcm; protein-L-isospartate O-methyltransferase [Nitrosomonas europaea ATCC 19718] emb|CAD83948.1| possible pcm; protein-L-isospartate O-methyltransferase [Nitrosomonas europaea ATCC 19718] Length = 218

322.3 Best-BlastP=>>nrprot No Hits found

3221.1 Best-BlastP=>>nrprot 62% Identities = 187/450 (41%), Positives = 275/450 (61%), Gaps = 16/450 (3%) ref|NP_819109.1| outer membrane protein TolC, putative [Coxiella burnetii RSA 493] Length = 616

3223.1 Best-BlastP=>>nrprot 74% Identities = 182/248 (73%), Positives = 212/248 (85%) ref|NP_820067.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 256

3224.3 Best-BlastP=>>nrprot 62% Identities = 316/713 (44%), Positives = 464/713 (65%), Gaps = 14/713 (1%) ref|NP_869762.1| probable sulfate transporter [Pirellula sp.] emb|CAD77140.1| probable sulfate transporter [Pirellula sp.] Length = 768

3226.2 Best-BlastP=>>nrprot 50% Identities = 28/64 (43%), Positives = 44/64 (68%) gb|AAP78483.1| C.Ahd1 [Aeromonas hydrophila] Length = 74

3228.1 Best-BlastP=>>nrprot 70% Identities = 40/66 (60%), Positives = 49/66 (74%) Gaps = 1/66 (1%) ref|ZP_00067276.1| COG1278: Cold shock proteins [Microbulbifer degradans 2-40] Length = 71

323.2 Best-BlastP=>>nrprot No Hits found

3230.1 Best-BlastP=>>nrprot No Hits found

3231.1 Best-BlastP=>>nrprot 56% Identities = 25/52 (48%), Positives = 31/52 (59%) ref|NP_143190.1| hypothetical protein PH11305 [Pyrococcus horikoshii] pir|A71001 hypothetical protein PH11305 - Pyrococcus horikoshii dbj|BAA30409.1| 252aa [long hypothetical protein Pyrococcus horikoshii] Length = 252

3232.1 Best-BlastP=>>nrprot No Hits found

3233.1 Best-BlastP=>>nrprot 19% Identities = 34/98 (34%), Positives = 52/98 (53%), Gaps = 1/98 (1%) ref|ZP_00106280.1| COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Nostoc punctiforme] Length = 210

3234.3 Best-BlastP=>>nrprot 53% Identities = 71/228 (31%), Positives = 125/228 (54%), Gaps = 1/228 (0%) ref|NP_9288824.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii] TTO1 emb|CAE13825.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii] TTO1 Length = 231

3235.3 Best-BlastP=>>nrprot 66% Identities = 89/162 (54%), Positives = 120/162 (74%) ref|NP_311228.1| hypothetical protein [Escherichia coli O157:H7] ref|NP_416820.1| orf, hypothetical protein [Escherichia coli K12] spt|P09548|DEDAA_ECOLI_DedA protein (DSG-1 protein) pir|XMECAD dedA protein - Escherichia coli (strain K-12) pir|A98029 hypothetical protein ECs3201 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) gb|AAC23964.1| dedA gb|AAC75377.1| orf, hypothetical protein [Escherichia coli K12] dbj|BAA16174.1| dedA protein [Escherichia coli] dbj|BAB36624.1| hypothetical protein [Escherichia coli O157:H7] Length = 219

3236.3 Best-BlastP=>>nrprot No Hits found

3238.1 Best-BlastP=>>nrprot 67% Identities = 134/263 (50%), Positives = 195/263 (74%), Gaps = 1/263 (0%) ref|NP_421700.1| conserved hypothetical protein [Caulobacter crescentus CB15] pir|H87608 conserved hypothetical protein CC2906 [imported] - Caulobacter crescentus gb|AAK24868.1| conserved hypothetical protein [Caulobacter crescentus CB15] Length = 289

3239.1 Best-BlastP=>>nrprot 58% Identities = 31/85 (36%), Positives = 57/85 (67%) Gaps = 2/85 (2%) ref|NP_820572.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 102

324.3 Best-BlastP=>>nrprot 72% Identities = 106/224 (47%), Positives = 160/224 (71%), Gaps = 5/224 (2%) ref|ZP_00045186.1| COG2200: FOG: EAL domain [Magnetococcus sp. MC-1] Length = 577

3240.3 Best-BlastP=>>nrprot 52% Identities = 24/64 (37%), Positives = 42/64 (65%) ref|NP_458973.1| Putative periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_463417.1| hyperosmotically inducible periplasmic protein, RpsS-dependent stationary phase gene [Salmonella typhimurium LT2] ref|NP_808176.1| Putative periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|AE1072 Putative periplasmic protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAL23376.1| hyperosmotically inducible periplasmic protein [Salmonella typhimurium LT2] emb|CAD03396.1| Putative periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO72036.1| Putative periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 205

3242.3 Best-BlastP=>>nrprot 14% Identities = 72/325 (22%), Positives = 126/325 (38%), Gaps = 37/325 (11%) gb|AAB96623.1| spheroidin [Heliothis armigera entomopoxvirus] Length = 1007

3243.1 Best-BlastP=>>nrprot No Hits found

3244.2 Best-BlastP=>>nrprot 60% Identities = 102/241 (42%), Positives = 153/241 (63%), Gaps = 2/241 (0%) ref|NP_465213.1| similar to glucose 1-dehydrogenase [Listeria monocytogenes EGDe] pir|AH1285 glucose 1-dehydrogenase homolog [mo1688 [imported]] - Listeria monocytogenes (strain EGDe) emb|CAC99766.1|mo1688 [Listeria monocytogenes] Length = 248

3246.2 Best-BlastP=>>nrprot 24% Identities = 100/360 (27%), Positives = 160/360 (44%), Gaps = 67/360 (18%) ref|NP_905966.1| conserved hypothetical protein [Porphyromonas gingivalis W83] gb|AAQ66865.1| conserved hypothetical protein [Porphyromonas gingivalis W83] Length = 339

3248.1 Best-BlastP=>>nrprot 38% Identities = 87/154 (56%), Positives = 114/154 (74%) ref|ZP_00111795.1| COG0784: FOG: CheY-like receiver [Nostoc punctiforme] Length = 557

3249.2 Best-BlastP=>>nrprot 13% Identities = 22/55 (40%), Positives = 29/55 (52%) ref|NP_798062.1| hypothetical protein VP1683 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC59946.1| hypothetical protein [Vibrio parahaemolyticus] Length = 325

3251.1 Best-BlastP=>>nrprot No Hits found

3250.1 Best-BlastP=>>nrprot No Hits found

3251.1 Best-BlastP=>>nrprot 48% Identities = 39/131 (29%), Positives = 65/131 (49%), Gaps = 3/131 (2%) emb|CAC05487.1| YcfB protein [Erwinia amylovora] Length = 132

3252.1 Best-BlastP=>>nrprot No Hits found

3257.2 Best-BlastP=>>nrprot 46% Identities = 40/122 (32%), Positives = 70/122 (57%), Gaps = 4/122 (3%) ref|NP_755556.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN82129.1|AE016766_217 Hypothetical protein [Escherichia coli CFT073] Length = 131

3258.2 Best-BlastP=>>nrprot 35% Identities = 70/225 (31%), Positives = 111/225 (49%), Gaps = 27/225 (12%) ref|NP_755557.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN82130.1|AE016766_218 Hypothetical protein [Escherichia coli CFT073] Length = 305

3260.2 Best-BlastP=>>nrprot No Hits found

3263.2 Best-BlastP=>>nrprot 61% Identities = 128/368 (34%), Positives = 227/368 (61%), Gaps = 10/368 (2%) ref|NP_819469.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO89983.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 428

3265.1 Best-BlastP=> >nrprot 65% Identities = 140/293 (47%), Positives = 195/293 (66%), Gaps = 2/293 (0%) ref|NP_820459.1| hydrogen peroxide-inducible genes activator OxyR [Coxiella burnetii RSA 493] Length = 311

3267.1 Best-BlastP=> >nrprot 50% Identities = 57/258 (22%), Positives = 104/258 (40%), Gaps = 75/258 (29%) ref|NP_797353.1| hypothetical protein VP0974 [Vibrio parahaemolyticus RIMD 22106333 dbj|BAC59237.1| hypothetical protein [Vibrio parahaemolyticus] Length = 269

3269.1 Best-BlastP=> >nrprot 55% Identities = 400/1113 (35%), Positives = 600/1113 (53%), Gaps = 64/1113 (5%) ref|NP_820225.1| UvrD/REP helicase family protein [Coxiella burnetii RSA 493] Length = 1110

327.2 Best-BlastP=> >nrprot 70% Identities = 364/616 (59%), Positives = 458/616 (74%), Gaps = 76/616 (1%) ref|ZP_00141174.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 645

3271.3 Best-BlastP=> >nrprot 46% Identities = 187/674 (27%), Positives = 308/674 (45%), Gaps = 55/674 (8%) ref|NP_437090.1| putative membrane-located cell surface saccharide saccharide acetylase protein [Sinorhizobium meliloti] pir|F95910 probable membrane-located cell surface saccharide saccharide acetylase protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb|CAC48950.1| putative membrane-located cell surface saccharide saccharide acetylase protein [Sinorhizobium meliloti] Length = 677

3272.1 Best-BlastP=> >nrprot 55% Identities = 49/148 (33%), Positives = 82/148 (55%), Gaps = 14/148 (9%) ref|NP_820842.1| conserved hypothetical protein [Coxiella burnetii RSA 493] qb|AAO91356.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 175

3273.1 Best-BlastP=> >nrprot 40% Identities = 34/95 (35%), Positives = 50/95 (52%), Gaps = 4/95 (4%) ref|NP_930855.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE16020.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii TTO1] Length = 175

3275.1 Best-BlastP=> >nrprot No Hits found

3276.2 Best-BlastP=> >nrprot No Hits found

3277.2 Best-BlastP=> >nrprot 61% Identities = 109/264 (41%), Positives = 165/264 (62%), Gaps = 5/264 (1%) ref|ZP_00055240.1| COG1073: Hydroases of the alpha/beta superfamily [Magnetospirillum magnetotacticum] Length = 297

3278.1 Best-BlastP=> >nrprot 28% Identities = 19/43 (44%), Positives = 28/43 (65%) ref|NP_523079.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD18671.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 232

328.1 Best-BlastP=> >nrprot 68% Identities = 161/292 (55%), Positives = 206/292 (70%), Gaps = 3/292 (1%) ref|NP_770597.1| 3-hydroxyisobutyrate dehydrogenase [Bradyrhizobium japonicum] dbj|BAC49222.1| 3-hydroxyisobutyrate dehydrogenase [Bradyrhizobium japonicum USDA 110] Length = 295

3280.1 Best-BlastP=> >nrprot 54% Identities = 101/267 (37%), Positives = 156/267 (58%), Gaps = 18/267 (6%) ref|NP_631554.1| conserved hypothetical protein [Streptomyces coelicolor A3(2)] emb|CAC44686.1| conserved hypothetical protein [Streptomyces coelicolor A3(2)] Length = 277

3281.1 Best-BlastP=> >nrprot No Hits found

3282.3 Best-BlastP=>>nrprot 82% Identities = 289/413 (69%), Positives = 341/413 (82%), Gaps = 4/413 (0%) ref|NP_819190.1| cell division protein FtsA [Coxiella burnetii RSA 493] gb|AAO89704.1| cell division protein FtsA [Coxiella burnetii RSA 493] Length = 410

3283.1 Best-BlastP=>>nrprot 50% Identities = 72/220 (32%), Positives = 120/220 (54%), Gaps = 1/220 (0%) ref|NP_253099.1| cell division protein FtsQ [Pseudomonas aeruginosa PA01] pir|B83094 cell division protein FtsQ PA4409 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAF26457.1| FtsQ [Pseudomonas aeruginosa] gb|AA004856_8 cell division protein FtsQ [Pseudomonas aeruginosa PA01] Length = 287

3285.3 Best-BlastP=>>nrprot 48% Identities = 106/303 (34%), Positives = 174/303 (57%), Gaps = 1/303 (0%) ref|ZP_00032705.1| COG0642: Signal transduction histidine kinase [Burkholderia fungorum] Length = 535

3288.3 Best-BlastP=>>nrprot 71% Identities = 120/221 (54%), Positives = 161/221 (72%) ref|ZP_00080602.1| COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Geobacter metallireducens] Length = 306

3290.1 Best-BlastP=>>nrprot No Hits found

3291.2 Best-BlastP=>>nrprot 77% Identities = 563/923 (60%), Positives = 715/923 (77%), Gaps = 5/923 (0%) ref|ZP_00066862.1| COG0525: Valyl-tRNA synthetase [Microbulbifer degradans 2-40] Length = 922

3295.2 Best-BlastP=>>nrprot 36% Identities = 75/282 (26%), Positives = 129/282 (45%), Gaps = 11/282 (3%) ref|NP_603055.1| 3-oxoacyl-[acyl]-carrier-protein synthase III [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb|AAL94354.1| 3-oxoacyl-[acyl]-carrier-protein synthase III [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 328

3297.3 Best-BlastP=>>nrprot 36% Identities = 36/137 (26%), Positives = 51/137 (37%), Gaps = 37/137 (27%) ref|ZP_00014317.1| hypothetical protein [Rhodospirillum rubrum] Length = 417

3299.3 Best-BlastP=>>nrprot 87% Identities = 711/878 (80%), Positives = 774/878 (88%), Gaps = 16/878 (1%) gb|AAG45149.1| TraA-like protein [Legionella pneumophila] Length = 883

330.2 Best-BlastP=>>nrprot 70% Identities = 267/493 (54%), Positives = 353/493 (71%), Gaps = 1/493 (0%) ref|NP_819940.1| methylmalonate-semialdehyde dehydrogenase [Coxiella burnetii RSA 493] gb|AAO90454.1| methylmalonate-semialdehyde dehydrogenase [Coxiella burnetii RSA 493] Length = 498

3301.2 Best-BlastP=>>nrprot 55% Identities = 261/488 (53%), Positives = 38/488 (7%) ref|NP_787151.1| propionyl-CoA carboxylase beta chain [Tropheryma whipplei TW0827] emb|CAD66717.1| propionyl-CoA carboxylase beta chain [Tropheryma whipplei TW0827] gb|AAO44120.1| propionyl-CoA carboxylase beta chain [Tropheryma whipplei str. TW0827] Length = 525

3303.2 Best-BlastP=>>nrprot No Hits found

3304.2 Best-BlastP=>>nrprot 50% Identities = 133/302 (44%), Positives = 189/302 (62%), Gaps = 7/302 (2%) ref|ZP_00043253.1| hypothetical protein [Magnetococcus sp. MC-1] Length = 831

3306.4 Best-BlastP=>>nrprot 29% Identities = 48/138 (34%), Positives = 71/138 (51%), Gaps = 13/138 (9%) ref|ZP_00052545.1| COG1020: Non-ribosomal peptide synthetase modules and related proteins [Magnetospirillum magnetotacticum] Length = 676

3307.4 Best-BlastP=>>nrprot No Hits found

3308.4 Best-BlastP=>>nrprot No Hits found

331.2 Best-BlastP=>>nrprot 69% Identities = 272/538 (50%), Positives = 371/538 (68%), Gaps = 5/538 (0%) ref|NP_406414.1| putative glutamine-dependent NAD [Yersinia pestis] ref|NP_668639.1| putative NH3-dependent NAD(+) synthetase [Yersinia pestis KIM] pir|AG0354 NAD synthase (glutamine-hydrolysing) (EC 6.3.5.1) - *Yersinia pestis* (strain CO92) emb|CAC92162.1| putative glutamine-dependent NAD [Yersinia pestis CO92] gb|AAM84890.1|AE013734_5 putative NH3-dependent NAD(+) synthetase [Yersinia pestis KIM] Length = 540

3311.1 Best-BlastP=>>nrprot 74% Identities = 275/459 (59%), Positives = 341/459 (74%), Gaps = 9/459 (1%) ref|NP_250486.1| cysteinyl-tRNA synthetase [Pseudomonas aeruginosa PA01] sp|Q9I2U7|SYC_PSEAE Cysteine-tRNA synthetase (Cysteine-tRNA ligase) (CysRS) pir|G83421 cysteinyl-tRNA synthetase PA1795 [Imported] - *Pseudomonas aeruginosa* (strain PAO1) gb|AAG05184.1|AE004605_6 cysteinyl-tRNA synthetase [Pseudomonas aeruginosa PAO1] Length = 460

3312.1 Best-BlastP=>>nrprot 32% Identities = 20/66 (30%), Positives = 34/66 (51%) ref|NP_759513.1| Unknown [Vibrio vulnificus CMCP6] gb|AAO09040.1|AE016798_200 Unknown [Vibrio vulnificus CMCP6] dbj|BAC93437.1| hypothetical protein [Vibrio vulnificus YJ016] Length = 103

3314.2 Best-BlastP=>>nrprot No Hits found

3316.1 Best-BlastP=>>nrprot 26% Identities = 80/363 (22%), Positives = 152/363 (41%), Gaps = 41/363 (11%) ref|NP_659473.1| hypothetical protein MGC33887 [Homo sapiens] gb|AAU49719.1|AF458591_1 hypothetical protein [Homo sapiens] Length = 590

3319.1 Best-BlastP=>>nrprot No Hits found

3322.2 Best-BlastP=>>nrprot 98% Identities = 265/269 (98%), Positives = 267/269 (99%) pir|T18335 icmG protein - *Legionella pneumophila* emb|CAA75166.1| icmG protein [Legionella pneumophila] gb|AAC38187.1|DotF [Legionella pneumophila] emb|CAA75332.1| icmG protein [Legionella pneumophila] Length = 269

3323.1 Best-BlastP=>>nrprot 99% Identities = 194/194 (100%), Positives = 194/194 (100%) pir|T18336 icmC protein - *Legionella pneumophila* emb|CAA75167.1| icmC protein [Legionella pneumophila] gb|AAC38186.1|DotE [Legionella pneumophila] emb|CAA75333.1| icmC protein [Legionella pneumophila] Length = 194

3324.1 Best-BlastP=>>nrprot 98% Identities = 130/132 (98%), Positives = 131/132 (99%) pir|T18337 icmD protein - *Legionella pneumophila* emb|CAA75168.1| icmD protein [Legionella pneumophila] emb|CA75334.1| icmD protein [Legionella pneumophila] Length = 132

3326.2 Best-BlastP=>>nrprot 99% Identities = 261/261 (100%), Positives = 261/261 (100%) gb|AAQ10306.1| DotU [Legionella pneumophila] Length = 261

3327.1 Best-BlastP=>>nrprot 46% Identities = 53/219 (24%), Positives = 99/219 (45%), Gaps = 19/219 (8%) ref|NP_840938.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD84775.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 343

3328.1 Best-BlastP=>>nrprot 70% Identities = 315/575 (54%), Positives = 407/575 (70%), Gaps = 5/575 (0%) ref|NP_252414.1| single-stranded-DNA-specific exonuclease RecJ [Pseudomonas aeruginosa PA01] pir|A83_81 single-stranded-DNA-specific exonuclease RecJ PA3725 [Imported] - *Pseudomonas aeruginosa* (strain PAO1) gb|AAG07112.1|AE004791_9 single-stranded-DNA-specific exonuclease RecJ [Pseudomonas aeruginosa PAO1] Length = 571

333.3 Best-BlastP=>>nrprot 57% Identities = 426/1088 (39%), Positives = 613/1088 (56%), Gaps = 70/1088 (6%) gb|AAP85938.1| putative helicase, superfamily II [Ralstonia eutropha] Length = 1106

3331.1 Best-BlastP=> >nrprot 61% Identities = 145/291 (49%), Positives = 203/291 (69%), Gaps = 1/291 (0%) ref|NP_719443.1| TIM-barrel protein, ybN family [Shewanella oneidensis MR-1] gb|AAN56887.1|AE015823_9 TIM-barrel protein, ybN family [Shewanella oneidensis MR-1] Length = 335

3333.1 Best-BlastP=> >nrprot 58% Identities = 52/122 (42%), Positives = 79/122 (64%), Gaps = 1/122 (0%) ref|NP_930852.1| Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (8-oxo-dGTPase) (dGTP pyrophosphorylase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16017.1| Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (8-oxo-dGTPase) (dGTP pyrophosphorylase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 130

3334.2 Best-BlastP=> >nrprot No Hits found

3336.2 Best-BlastP=> >nrprot No Hits found

3337.2 Best-BlastP=> >nrprot No Hits found

3338.1 Best-BlastP=> >nrprot No Hits found

3345.5 Best-BlastP=> >nrprot 42% Identities = 272/697 (39%), Positives = 416/697 (59%), Gaps = 23/697 (3%) ref|NP_440178.1| regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] pir|S74707 nitrogen fixation positive activator protein - Synechocystis sp. (strain PCC 6803) dbj|BAA16858.1| regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] Length = 840

3341.2 Best-BlastP=> >nrprot No Hits found

3343.1 Best-BlastP=> >nrprot No Hits found

3345.2 Best-BlastP=> >nrprot 17% Identities = 53/272 (19%), Positives = 137/272 (50%), Gaps = 28/272 (10%) ref|NP_701067.1| hypothetical protein [Plasmodium falciparum 3D7] gb|AAN35791.1|AE014838_69 hypothetical protein [Plasmodium falciparum 3D7] Length = 964

3346.2 Best-BlastP=> >nrprot 28% Identities = 105/343 (30%), Positives = 168/343 (48%), Gaps = 60/343 (17%) ref|NP_623492.1| Cell division protein FtsI/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] gb|AAM25096.1| Cell division protein FtsI/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] Length = 553

3347.1 Best-BlastP=> >nrprot 94% Identities = 239/266 (89%), Positives = 251/266 (94%) emb|CAC35728.1| OXA-29 [Fluoribacter gormanii] Length = 266

3348.2 Best-BlastP=> >nrprot 31% Identities = 115/295 (38%), Positives = 170/295 (57%), Gaps = 15/295 (5%) ref|ZP_00119503.1| COG0726: Predicted xylanase/chitin deacetylase [Cytophaga hutchinsonii] Length = 314

3349.3 Best-BlastP=> >nrprot 45% Identities = 72/238 (30%), Positives = 130/238 (54%), Gaps = 8/238 (3%) ref|NP_6388901.1| conserved hypothetical protein [Xanthomonas campestris campestris pv. campestris str. ATCC 33913] gb|AAM42825.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 314

335.1 Best-BlastP=> >nrprot 67% Identities = 115/207 (55%), Positives = 145/207 (70%), Gaps = 2/207 (0%) ref|NP_903041.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61035.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 206

3350.3 Best-BlastP=> >nrprot 41% Identities = 33/101 (32%), Positives = 50/101 (49%), Gaps = 3/101 (2%) ref|ZP_00116659.1| COG0346: Lactoylglutathione lyase and related lyases [Cytophaga hutchinsonii] Length = 150

3351.3 Best-BlastP=> >nrprot 30% Identities = 88/194 (45%), Positives = 121/194 (62%), Gaps = 1/194 (0%) ref[NP_531634.1] methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] pir[AH2691 methyltransferase Atu0936 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb[AAL41950.1] methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 202

3352.1 Best-BlastP=> >nrprot 42% Identities = 52/109 (47%), Positives = 67/109 (61%), Gaps = 6/109 (5%) ref[NP_819444.1] acetyltransferase, GNAT family [Coxiella burnetii RSA 493] gb[AAO89958.1] acetyltransferase, GNAT family [Coxiella burnetii RSA 493] Length = 118

3353.1 Best-BlastP=> >nrprot 48% Identities = 157/467 (33%), Positives = 245/467 (52%), Gaps = 16/467 (3%) ref[NP_417114.1] hypothetical protein [Escherichia coli K12] spi[PP52124|YFJ|_ECOLI] Hypothetical protein yfJ, pir[T08637 hypothetical protein b2625 - Escherichia coli (strain K-12) gb[AA79794.1] ORF_0469 gb[AAC75673.1] orf, hypothetical protein [Escherichia coli K12] Length = 469

3354.1 Best-BlastP=> >nrprot 47% Identities = 58/190 (30%), Positives = 91/190 (47%), Gaps = 2/190 (1%) gb[AAD53919.1|AF179611_3 pyridoxamine 5'-phosphate oxidase [Zymomonas mobilis]] Length = 192

3355.2 Best-BlastP=> >nrprot 72% Identities = 53/94 (56%), Positives = 70/94 (74%), Gaps = 1/94 (1%) gb[AAL55698.1|AF246719_2 hypothetical protein [Escherichia coli]] Length = 95

3356.2 Best-BlastP=> >nrprot 70% Identities = 44/83 (53%), Positives = 59/83 (71%) ref[NP_232869.1] conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir[EE82456 conserved hypothetical protein VCA0477 [imported] - Vibrio cholerae (strain N16961) serogroup O1] gb[AAF96381.1] conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 90

3357.2 Best-BlastP=> >nrprot No Hits found

3359.2 Best-BlastP=> >nrprot 48% Identities = 221/706 (31%), Positives = 362/706 (51%), Gaps = 53/706 (7%) ref[NP_820588.1] membrane protein, putative [Coxiella burnetii RSA 493] gb[AAO91102.1] membrane protein, putative [Coxiella burnetii RSA 493] Length = 698

336.1 Best-BlastP=> >nrprot 69% Identities = 186/324 (57%), Positives = 230/324 (70%), Gaps = 2/324 (0%) ref[NP_384292.1] PHOSPHATE TRANSPORT TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] spi[O30499|PIT_RHIME Probable low-affinity inorganic phosphate transporter gb[AB70171.1] phosphate transport protein [Sinorhizobium meliloti] emb[CAC41573.1] PHOSPHATE TRANSPORT TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] Length = 334

3360.1 Best-BlastP=> >nrprot No Hits found

3362.1 Best-BlastP=> >nrprot 43% Identities = 68/209 (32%), Positives = 106/209 (50%), Gaps = 5/209 (2%) ref[NP_178286.1] membrane protein - related [Arabidopsis thaliana] pir[H84428 probable membrane protein [imported] - Arabidopsis thaliana] gb[AA[D12695.1] putative membrane protein [Arabidopsis thaliana]] Length = 250

3363.2 Best-BlastP=> >nrprot 64% Identities = 148/300 (49%), Positives = 204/300 (68%), Gaps = 11/300 (3%) gb[AAC64375.1] thiamine synthase homolog [Botryotinia fuckeliana] Length = 342

3365.2 Best-BlastP=> >nrprot 66% Identities = 173/347 (49%), Positives = 238/347 (68%), Gaps = 13/347 (3%) ref[NP_819373.1] thiamine biosynthesis oxidoreductase ThIO, putative [Coxiella burnetii RSA 493] gb[AAO89887.1] thiamine biosynthesis oxidoreductase ThIO, putative [Coxiella burnetii RSA 493] Length = 338

3367.1 Best-BlastP=>>nrprot 41% Identities = 81/269 (30%), Positives = 123/269 (45%), Gaps = 20/269 (7%) emb|CAC17409.1| 3'-nucleotidase/nuclease [Leishmania mexicana] Length = 378

3368.2 Best-BlastP=>>nrprot No Hits found

337.2 Best-BlastP=>>nrprot 67% Identities = 241/457 (52%), Positives = 311/457 (68%), Gaps = 4/457 (0%) ref|NP_830123.1| Amino acid permease [Bacillus cereus ATCC 14579] gb|AAP07324.1| Amino acid permease [Bacillus cereus ATCC 14579] Length = 471

3371.2 Best-BlastP=>>nrprot 83% Identities = 321/438 (73%), Positives = 372/438 (84%) ref|NP_819599.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90113.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 439

3374.1 Best-BlastP=>>nrprot 25% Identities = 60/222 (27%), Positives = 94/222 (42%), Gaps = 21/222 (9%) ref|NP_774046.1| bII7406 [Bradyrhizobium japonicum] dbj|BAC52671.1| bII7406 [Bradyrhizobium japonicum USDA 110] Length = 300

3376.1 Best-BlastP=>>nrprot 30% Identities = 62/236 (26%), Positives = 106/236 (44%), Gaps = 15/236 (6%) ref|NP_819950.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90464.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 465

3378.2 Best-BlastP=>>nrprot 56% Identities = 210/580 (36%), Positives = 331/580 (57%), Gaps = 9/580 (1%) gb|AAC44717.1| FrgA [Legionella pneumophila] Length = 575

3385.1 Best-BlastP=>>nrprot 74% Identities = 252/254 (99%), Positives = 254/254 (100%) gb|AAM00642.1| essential conserved GTPase [Legionella pneumophila] Length = 254

3386.1 Best-BlastP=>>nrprot 77% Identities = 62/85 (72%), Positives = 72/85 (84%) ref|NP_636525.1| 50S ribosomal protein L27 [Xanthomonas campestris pv. campestris str. ATCC 33913] sp|Q8PBH1|RL27_XANCP 50S ribosomal protein L27 gb|AAM40449.1| 50S ribosomal protein L27 [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 86

3388.1 Best-BlastP=>>nrprot 28% Identities = 65/168 (38%), Positives = 105/168 (62%), Gaps = 1/168 (0%) ref|ZP_00125980.1| COG2199: FOG: GGDEF domain [Pseudomonas syringae pv. syringae B728a] Length = 972

3389.1 Best-BlastP=>>nrprot 68% Identities = 149/315 (47%), Positives = 222/315 (70%) ref|ZP_00068004.1| COG0142: Geranylgeranyl pyrophosphate synthase [Microbulbifer degradans 2-40] Length = 320

339.4 Best-BlastP=>>nrprot 89% Identities = 168/194 (86%), Positives = 174/194 (89%), Gaps = 8/194 (4%) gb|AAK52070.1| Rcp [Legionella pneumophila] Length = 186

3390.1 Best-BlastP=>>nrprot 37% Identities = 21/61 (34%), Positives = 32/61 (52%) ref|NP_820745.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91259.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 72

3391.2 Best-BlastP=>>nrprot 99% Identities = 748/751 (99%) gb|AAN17185.1|AF492466_3 ferrous iron transporter B [Legionella pneumophila] Length = 751

3394.1 Best-BlastP=>>nrprot No Hits found

3395.2 Best-BlastP=>>nrprot No Hits found

3396.1 Best-BlastP=>>nrprot No Hits found

3397.1 Best-BlastP=>>nrprot 62% Identities = 72/167 (43%), Positives = 106/167 (63%), Gaps = 6/167 (3%) ref|NP_840350.1| putative antirestriction protein [Nitrosomonas europaea ATCC 19718] emb|CAD84171.1| putative antirestriction protein [Nitrosomonas europaea ATCC 19718] Length = 171

3398.1 Best-BlastP=> >nrprot 61% Identities = 58/145 (40%), Positives = 87/145 (60%), Gaps = 7/145 (4%) ref|NP_252922.1| single-stranded DNA-binding protein [Pseudomonas aeruginosa PA01] sp|P40947|SSB_PSEAE Single-strand binding protein (SSB) (Helix-destabilizing protein) pir|S44302 single-stranded DNA-binding protein - Pseudomonas aeruginosa emb|CAA83688.1| single-stranded DNA binding protein [Pseudomonas aeruginosa] gb|AAG07620.1|AE004840_6 single-stranded DNA-binding protein [Pseudomonas aeruginosa PA01] Length = 165

3399.1 Best-BlastP=> >nrprot No Hits found

34.1 Best-BlastP=> >nrprot No Hits found

3401.2 Best-BlastP=> >nrprot No Hits found

3402.2 Best-BlastP=> >nrprot 53% Identities = 108/298 (36%), Positives = 160/298 (53%), Gaps = 14/298 (4%) ref|NP_862370.1| unknown [Francisella tularensis subsp. novicida] gb|AAD17308.1| unknown [Francisella tularensis subsp. novicida] Length = 292

3404.2 Best-BlastP=> >nrprot 31% Identities = 51/187 (27%), Positives = 86/187 (45%), Gaps = 9/187 (4%) ref|ZP_00091084.1| COG0582: Integrase [Azotobacter vinelandii] Length = 287

3406.2 Best-BlastP=> >nrprot 34% Identities = 46/197 (23%), Positives = 76/197 (38%), Gaps = 13/197 (6%) ref|NP_466297.1| hypothetical membrane protein [Listeria monocytogenes EGD-e] pir|AF1421 hypothetical membrane protein Imo2775 [imported] - Listeria EGD-e) emb|CAD00988.1| Imo2775 [Listeria monocytogenes] Length = 722

341.6 Best-BlastP=> >nrprot 99% Identities = 141/141 (100%), Positives = 141/141 (100%), Gaps = 0/141 (0%) ref|AAC44222.1| hemin binding protein Hbp [Legionella pneumophila] Length = 141

3411.2 Best-BlastP=> >nrprot 20% Identities = 42/162 (25%), Positives = 75/162 (46%), Gaps = 10/162 (6%) ref|NP_871522.1| rplA [Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis] sp|Q8D236|RL1_WIGBR 50S ribosomal protein L1 dbj|BAC244665.1| rplA [Wigglesworthia brevipalpis] Length = 242

3413.2 Best-BlastP=> >nrprot 49% Identities = 76/296 (25%), Positives = 150/296 (50%), Gaps = 16/296 (5%) ref|NP_832129.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] gb|AAP09330.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] Length = 300

3414.3 Best-BlastP=> >nrprot 33% Identities = 115/406 (28%), Positives = 184/406 (45%), Gaps = 47/406 (11%) ref|ZP_00112010.1| COG0666: FOG: Ankyrin repeat [Nostoc punctiforme] Length = 427

3415.2 Best-BlastP=> >nrprot 38% Identities = 48/154 (31%), Positives = 69/154 (44%), Gaps = 14/154 (9%) ref|NP_740808.1| dotH Histone Methyltransferase (1C952) [Caenorhabditis elegans] gb|AAK39620.2| Hypothetical protein Y39G10AR.18a [Caenorhabditis elegans] = 1015

3416.1 Best-BlastP=> >nrprot 73% Identities = 65/99 (65%), Positives = 76/99 (76%) ref|NP_820718.1| integration host factor, beta subunit [Coxiella burnetii RSA 493] Length = 112

3417.1 Best-BlastP=> >nrprot 91% Identities = 155/191 (81%), Positives = 172/191 (90%), Gaps = 3/191 (1%) ref|NP_780077.1| deoxycytidine triphosphate deaminase [Xylella fastidiosa Temecula1] sp|Q87AD1|DCD_XYLFT Deoxycytidine triphosphate deaminase (dCTP deaminase) gb|AAO29726.1| deoxycytidine triphosphate deaminase [Xylella fastidiosa Temecula1] Length = 191

3418.1 Best-BlastP=> >nrprot 99% Identities = 283/283 (100%), Positives = 283/283 (100%) ref|AAC83338.1| major outer membrane protein precursor [Legionella pneumophila] gb|AAC83342.1| major outer membrane protein precursor [Legionella pneumophila] Length = 289

3419.3 Best-BlastP=>>nrprot 36% Identities = 47/225 (20%), Positives = 93/225 (41%), Gaps = 37/225 (16%) ref|NP_703974.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7] emb|CAD50587.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7] Length = 2879

342.2 Best-BlastP=>>nrprot 74% Identities = 237/407 (58%), Positives = 310/407 (76%) ref|NP_924319.1| probable aminotransferase [Gloeobacter violaceus] dbj|BAC89314.1| glr1373 [Gloeobacter violaceus] Length = 417

3421.2 Best-BlastP=>>nrprot 27% Identities = 56/257 (21%), Positives = 108/257 (42%), Gaps = 32/257 (12%) ref|NP_705457.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD52694.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1179

3423.3 Best-BlastP=>>nrprot 86% Identities = 335/366 (91%), Positives = 346/366 (94%) gb|AAL23711.1| RaIf [Legionella pneumophila] Length = 374

3426.1 Best-BlastP=>>nrprot 33% Identities = 56/142 (39%), Positives = 78/142 (54%), Gaps = 2/142 (1%) ref|NP_108258.1| hypothetical protein [Mesorhizobium loti] dbj|BAB53719.1| hypothetical protein [Mesorhizobium loti] Length = 285

3428.1 Best-BlastP=>>nrprot 47% Identities = 72/233 (30%), Positives = 129/233 (55%), Gaps = 2/233 (0%) ref|ZP_00006345.1| COG1409: Predicted phosphohydrolases [Rhodobacter sphaeroides] Length = 273

3429.1 Best-BlastP=>>nrprot 33% Identities = 126/638 (19%), Positives = 247/638 (38%), Gaps = 85/638 (13%) gb|EAA15312.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 1527

343.1 Best-BlastP=>>nrprot 70% Identities = 78/139 (56%), Positives = 106/139 (76%) ref|NP_924320.1| hypothetical protein glr1374 [Gloeobacter violaceus] dbj|BAC89315.1| glr1374 [Gloeobacter violaceus] Length = 148

3431.3 Best-BlastP=>>nrprot 39% Identities = 109/279 (39%), Positives = 169/279 (60%), Gaps = 8/279 (2%) ref|ZP_00023400.1| COG2056: Predicted permease [Ralstonia metallidurans] Length = 325

3432.2 Best-BlastP=>>nrprot 63% Identities = 161/334 (48%), Positives = 218/334 (65%) ref|NP_346834.1| Similar to chloromuconate cycloisomerase [Clostridium acetobutylicum] pir|C96923 similar to chloromuconate cycloisomerase [imported] - Clostridium acetobutylicum gb|AAK78174.1|AE007532_7 Similar to chloromuconate cycloisomerase [Clostridium acetobutylicum] Length = 358

3437.1 Best-BlastP=>>nrprot 32% Identities = 79/336 (23%), Positives = 125/336 (37%), Gaps = 58/336 (17%) ref|NP_523168.1| PROBABLE ACID SPHINGOMYELINASE-LIKE PHOSPHODIESTERASE TRANSMEMBRANE PROBABLE ACID SPHINGOMYELINASE-LIKE PHOSPHODIESTERASE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD18760.1| Length = 476

3441.1 Best-BlastP=>>nrprot 67% Identities = 58/107 (54%), Positives = 76/107 (71%) ref|ZP_00096500.1| COG2151: Predicted metal-sulfur cluster biosynthetic enzyme [Novosphingobium aromaticivorans] Length = 160

3442.3 Best-BlastP=>>nrprot 41% Identities = 160/450 (35%), Positives = 247/450 (54%), Gaps = 6/450 (1%) ref|NP_819065.1| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase [Coxiella burnetii RSA 493] gb|AAO89579.1| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase [Coxiella burnetii RSA 493] Length = 477

3443.1 Best-BlastP=>>nrprot 64% Identities = 112/252 (44%), Positives = 170/252 (67%) ref|ZP_00091089.1| COG1475: Predicted transcriptional regulators [Azotobacter vinelandii] Length = 294

3444.1 Best-BlastP=>>nrprot No Hits found

3445.3 Best-BlastP=>>nrprot 53% Identities = 141/332 (42%), Positives = 185/332 (55%), Gaps = 16/332 (4%) ref|ZP_00140422.1| COG1652:
Uncharacterized protein containing LysM domain [Pseudomonas aeruginosa UCBPP-PA14] Length = 371

3446.1 Best-BlastP=>>nrprot 56% Identities = 158/291 (54%), Positives = 205/291 (70%), Gaps = 3/291 (1%) ref|NP_820973.1| DNA processing protein DprA, putative [Coxiella burnetii RSA 493] gb|AO91487.1| DNA processing protein DprA, putative [Coxiella burnetii RSA 493] Length = 308

3447.1 Best-BlastP=>>nrprot 43% Identities = 30/121 (24%), Positives = 64/121 (52%), Gaps = 5/121 (4%) ref|NP_484103.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AC1814 hypothetical protein all0059 [imported] - Nostoc sp. (strain PCC 7120) db|BAB77583.1| ORF_ID all0059~hypothetical protein [Nostoc sp. PCC 7120] Length = 727

3450.2 Best-BlastP=>>nrprot 73% Identities = 202/344 (58%), Positives = 264/344 (76%), Gaps = 1/344 (0%) ref|NP_469414.1| similar to E. coli Ada protein (O6-methylguanine-DNA methyltransferase) [Listeria innocua] pir|AE1441 E. coli Ada protein (O6-methylguanine-DNA methyltransferase) homolog lin0068 [imported] - Listeria innocua (strain Cili11262) emb|CAC95301.1| lin0068 [Listeria innocua] Length = 350

3451.1 Best-BlastP=>>nrprot No Hits found

3453.1

3453.2 Best-BlastP=>>nrprot 10% Identities = 40/127 (31%), Positives = 53/127 (41%), Gaps = 19/127 (14%) ref|NP_356305.1| AGR_L_1030p [Agrobacterium tumefaciens] ref|NP_534828.1| hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AB3091 hypothetical protein Atu4350 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) gb|AAK89090.1| AGR_L_1030p hypothetical protein AGR_L_1030 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) gb|AAK89090.1| AGR_L_1030p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAU45144.1| hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 278

3454.1 Best-BlastP=>>nrprot 42% Identities = 31/137 (22%), Positives = 62/137 (45%), Gaps = 21/137 (15%) ref|NP_832446.1| Acetyltransferase [Bacillus cereus ATCC 14579] gb|AAP09647.1| Acetyltransferase [Bacillus cereus ATCC 14579] Length = 141

3455.3 Best-BlastP=>>nrprot No Hits found

3456.4 Best-BlastP=>>nrprot 70% Identities = 83/166 (50%), Positives = 119/166 (71%), Gaps = 7/166 (4%) ref|ZP_00012554.1| COG3158: K+ transporter [Rhodopseudomonas palustris] Length = 620

3459.3 Best-BlastP=>>nrprot 57% Identities = 189/475 (39%), Positives = 283/475 (59%), Gaps = 7/475 (1%) gb|AAP85869.1| putative potassium uptake protein [Ralstonia eutropha] Length = 632

346.2 Best-BlastP=>>nrprot 67% Identities = 160/326 (49%), Positives = 216/326 (66%), Gaps = 11/326 (3%) sp|Q9KNS6|SYK3_VIBCH Putative lysyl-tRNA synthetase (Lysine--tRNA ligase) (LysRS) (GX) Length = 324

3461.4 Best-BlastP=>>nrprot 18% Identities = 67/286 (23%), Positives = 116/286 (40%), Gaps = 45/286 (15%) gb|EAA19312.1| heat shock protein hsp70 homologue Pfhsp70-3 [Plasmodium yoelii] Length = 663

3463.1 Best-BlastP=>>nrprot 84% Identities = 199/269 (73%), Positives = 233/269 (86%) ref|ZP_00103515.1| COG2877: 3-deoxy-D-manno-octulonic acid (KDO) 8-phosphate synthase [Desulfitobacterium hafniense] Length = 277

3465.2 Best-BlastP=>>nrprot 84% Identities = 371/544 (68%), Positives = 460/544 (84%), Gaps = 1/544 (0%) ref|ZP_00067534.1| COG0504: CTP synthase (UTP-ammonia lyase) [Microbulbifer degradans 2-40] Length = 543

3466.1 Best-BlastP=>>nrprot 61% Identities = 28/60 (46%), Positives = 41/60 (68%), Gaps = 2/60 (3%) ref|NP_908035.1| HYPOTHETICAL PROTEIN- Putative Site-specific recombinase [Wolinella succinogenes] emb|CAE10935.1| HYPOTHETICAL PROTEIN-Putative Site-specific recombinase [Wolinella succinogenes] Length = 207

3468.2 Best-BlastP=>>nrprot 78% Identities = 236/412 (57%), Positives = 320/412 (77%), Gaps = 14/412 (3%) pir|S42875 dihydroliopamide S- succinyltransferase (EC 2.3.1.61) - *Coxiella burnetii* emb|CAA54875.1| putative dihydroliopamide succinyltransferase [Coxiella burnetii] Length = 405

347.1 Best-BlastP=>>nrprot 60% Identities = 119/292 (40%), Positives = 182/292 (62%), Gaps = 1/292 (0%) ref|ZP_00055839.1| COG2933: Predicted SAM-dependent methyltransferase [Magnetospirillum magnetotacticum] Length = 324

3472.1 Best-BlastP=>>nrprot 27% Identities = 26/50 (52%), Positives = 28/50 (56%), Gaps = 10/50 (20%) ref|NP_773097.1| b|6457 [Bradyrhizobium japonicum] dbj|BAC51722.1| b|6457 [Bradyrhizobium japonicum USDA 110] Length = 254

3473.1 Best-BlastP=>>nrprot No Hits found

3476.1 Best-BlastP=>>nrprot 63% Identities = 160/356 (44%), Positives = 238/356 (66%) ref|NP_819753.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAC90267.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 377

3477.2 Best-BlastP=>>nrprot 76% Identities = 140/241 (58%), Positives = 187/241 (77%) ref|NP_819754.1| ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] gb|AAQ90268.1| ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] Length = 268

3480.4 Best-BlastP=>>nrprot 56% Identities = 185/551 (33%), Positives = 314/551 (56%), Gaps = 12/551 (2%) ref|NP_441242.1| hypothetical protein [Synechocystis sp. PCC 6803] pir|S75060 conserved hypothetical protein sli1595 - Synechocystis sp. (strain ORF_ID:sli1595~hypothetical protein [Synechocystis sp. PCC 6803] Length = 568

3481.2 Best-BlastP=>>nrprot 67% Identities = 38/89 (42%), Positives = 61/89 (68%), Gaps = 1/89 (1%) ref|NP_442504.1| PCC7942 clock gene...ORFE [Synechocystis sp. PCC 6803] pir|S76630 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10574.1| sli0486 [Synechocystis sp. PCC 6803] Length = 102

3483.3 Best-BlastP=>>nrprot 52% Identities = 71/196 (36%), Positives = 106/196 (54%), Gaps = 7/196 (3%) ref|NP_216630.1| hypothetical protein Rv2114 [Mycobacterium tuberculosis H37Rv] ref|NP_855787.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] pir|E70512 hypothetical protein Rv2114 - Mycobacterium tuberculosis (strain H37RV) emb|CAB10705.1| hypothetical protein Rv2114 [Mycobacterium tuberculosis H37Rv] emb|CAD96991.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] Length = 207

3484.1 Best-BlastP=>>nrprot No Hits found

3485.1 Best-BlastP=>>nrprot No Hits found

3486.1 Best-BlastP=>>nrprot No Hits found

3488.1 Best-BlastP=>>nrprot 16% Identities = 52/260 (20%), Positives = 116/260 (44%), Gaps = 26/260 (10%) pir|T14867 interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| interaptin [Dictyostelium discoideum] Length = 1738

3489.2 Best-BlastP=>>nrprot 22% Identities = 37/178 (20%), Positives = 74/178 (41%), Gaps = 13/178 (7%) ref|NP_624872.1| hypothetical protein SCF73.06c [Streptomyces coelicolor A3(2)] emb|CAB5741.1| hypothetical protein SCF73.06c [Streptomyces coelicolor A3(2)] Length = 333

349.2 Best-BlastP=> >nrprot 66% Identities = 109/211 (51%), Positives = 1/211 (0%) ref|ZP_00013996.1| COG2872: Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain [Rhodospirillum rubrum] Length = 214

3494.2 Best-BlastP=> >nrprot 55% Identities = 41/85 (48%), Positives = 58/85 (68%) ref|ZP_00015213.1| COG2823: Predicted periplasmic or secreted lipoprotein [Rhodospirillum rubrum] Length = 104

3496.2 Best-BlastP=> >nrprot 30% Identities = 37/120 (30%), Positives = 50/120 (41%), Gaps = 24/120 (20%) ref|NP_827755.1| hypothetical protein [Streptomyces avermitilis MA-4680] dbj|BAC74290.1| hypothetical protein [Streptomyces avermitilis MA-4680] Length = 574

3498.1 Best-BlastP=> >nrprot No Hits found

3499.1 Best-BlastP=> >nrprot No Hits found

35.1 Best-BlastP=> >nrprot 98% Identities = 262/265 (98%), Positives = 262/265 (98%) emb|CAB60063.1| lvrE [Legionella pneumophila] Length = 265

350.3 Best-BlastP=> >nrprot 25% Identities = 29/124 (23%), Positives = 50/124 (40%), Gaps = 12/124 (9%) gb|AAD40638.1|AF128842_1 extracellular calcium-sensing receptor [Mus musculus] Length = 1079

3500.3 Best-BlastP=> >nrprot 30% Identities = 61/283 (21%), Positives = 120/283 (42%), Gaps = 16/283 (5%) ref|NP_928738.1| hypothetical protein [Photobacterium luminescens subsp. laumondii TTO1] embl|CAE13733.1| unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] Length = 417

3502.3 Best-BlastP=> >nrprot 55% Identities = 57/145 (39%), Positives = 91/145 (62%), Gaps = 5/145 (3%) pir|JQ0144 probable protein-disulfide oxidoreductase (EC 1.8.4.-) - Pseudomonas aeruginosa Length = 163

3503.2 Best-BlastP=> >nrprot 74% Identities = 229/383 (59%), Positives = 287/383 (74%) ref|NP_820071.1| queuine tRNA-ribosyltransferase [Coxiella burnetii RSA 493] gb|AAQ90585.1| queuine tRNA-ribosyltransferase [Coxiella burnetii RSA 493] Length = 385

3504.1 Best-BlastP=> >nrprot 98% Identities = 163/164 (99%), Positives = 163/164 (99%) pir|S49314| peptidylprolyl isomerase (EC 5.2.1.8) - Legionella pneumophila emb|CAA58722.1| cyclophilin [Legionella pneumophila] Length = 164

3506.1 Best-BlastP=> >nrprot 69% Identities = 116/212 (54%), Positives = 146/212 (68%), Gaps = 4/212 (1%) ref|NP_245872.1| unknown [Pasteurellales multocida] gb|AAK03019.1| unknown [Pasteurella multocida] Length = 226

3507.1 Best-BlastP=> >nrprot 52% Identities = 29/123 (23%), Positives = 60/123 (48%), Gaps = 8/123 (6%) gb|EAA21917.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 296

3508.2 Best-BlastP=> >nrprot 61% Identities = 43/94 (45%), Positives = 61/94 (64%) ref|ZP_00088933.1| COG0640: Predicted transcriptional regulators [Azotobacter vinelandii] Length = 107

3509.2 Best-BlastP=> >nrprot 15% Identities = 31/117 (26%), Positives = 55/117 (47%) ref|XP_306772.1| ENSANGP000000000282 [Anopheles gambiae] gb|EAA02010.2| ENSANGP000000000282 [Anopheles gambiae str. PEST] Length = 210

351.1 Best-BlastP=> >nrprot 59% Identities = 52/141 (36%), Positives = 89/141 (63%), Gaps = 6/141 (4%) ref|NP_562901.1| conserved hypothetical protein [Clostridium perfringens] dbj|BAB81691.1| conserved hypothetical protein [Clostridium perfringens str. 13] Length = 168

3511.2 Best-BlastP=> >nrprot 61% Identities = 160/368 (43%), Positives = 237/368 (64%) ref|NP_902574.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 377

3512.1 Best-BlastP=> >nrprot 13% Identities = 37/145 (25%), Positives = 72/145 (49%), Gaps = 9/145 (6%) dbj|BAB62990.1| hypothetical protein [Macaca fascicularis] Length = 533

3514.1 Best-BlastP=> >nrprot No Hits found

3515.2 Best-BlastP=> >nrprot 25% Identities = 28/85 (32%), Positives = 42/85 (49%), Gaps = 4/85 (4%) ref|NP_745177.1| pyocin R2_PP, transcriptional repressor, C1/C2 family [Pseudomonas putida KT2440] gb|AAN68641.1|AE016494.1 pyocin R2_PP, transcriptional repressor, C1/C2 family [Pseudomonas putida KT2440] Length = 243

3516.2 Best-BlastP=> >nrprot 53% Identities = 25/56 (44%), Positives = 38/56 (67%) ref|NP_246251.1| unknown [Pasteurella multocida] spl|Q9GLC6|YD13_PASMU Hypothetical UFP0235 protein PM1313 gb|AAK03397.1| unknown [Pasteurella multocida] Length = 99

3517.3 Best-BlastP=> >nrprot 56% Identities = 135/383 (35%), Positives = 219/383 (57%), Gaps = 2/383 (0%) ref|NP_820467.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO0981.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 428

3519.1 Best-BlastP=> >nrprot 31% Identities = 80/231 (34%), Positives = 124/231 (53%), Gaps = 7/231 (3%) ref|NP_828099.1| putative glycosyl transferase [Streptomyces avermitilis MA-4680] dbj|BAC74634.1| putative glycosyl transferase [Streptomyces avermitilis MA-4680] Length = 265

3520.1 Best-BlastP=> >nrprot 33% Identities = 90/291 (30%), Positives = 153/291 (52%), Gaps = 5/291 (1%) ref|ZP_00056311.1| COG1807: 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family [Magnetospirillum magnetotacticum] Length = 500

3521.2 Best-BlastP=> >nrprot 38% Identities = 88/281 (31%), Positives = 147/281 (52%), Gaps = 16/281 (5%) ref|NP_561543.1| probable choline kinase [Clostridium perfringens] dbj|BAB80333.1| probable choline kinase [Clostridium perfringens str. 13] Length = 622

3522.1 Best-BlastP=> >nrprot 70% Identities = 143/261 (54%), Positives = 180/261 (68%), Gaps = 11/261 (4%) ref|ZP_00022284.1| COG3298: Predicted 3'-5' exonuclease related to the exonuclease domain of PolB [Ralstonia metallidurans] Length = 278

3524.1 Best-BlastP=> >nrprot 67% Identities = 76/142 (53%), Positives = 97/142 (68%) ref|ZP_00065344.1| COG4764: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] Length = 204

3525.1 Best-BlastP=> >nrprot 78% Identities = 137/218 (62%), Positives = 171/218 (78%) ref|NP_888550.1| adenylylate kinase [Bordetella bronchiseptica] emb|CAE32502.1| adenylylate kinase [Bordetella bronchiseptica] Length = 218

3527.1 Best-BlastP=> >nrprot 63% Identities = 50/115 (43%), Positives = 77/115 (66%) ref|ZP_00042420.1| COG0526: Thiol-disulfide isomerase and thioredoxins [Magnetococcus sp. MC-1] Length = 124

3530.1 Best-BlastP=> >nrprot No Hits found

3532.1 Best-BlastP=> >nrprot 25% Identities = 141/689 (20%), Positives = 276/689 (40%), Gaps = 124/689 (17%) ref|NP_048227.1| ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] pir|T28317 ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus gb|AAC97677.1| ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] Length = 1127

3533.1 Best-BlastP=> >nrprot 81% Identities = 155/205 (75%), Positives = 173/205 (84%) ref|NP_819890.1| uridine kinase [Coxiella burnetii RSA 493] gb|AAO90404.1| uridine kinase [Coxiella burnetii RSA 493] Length = 215

3534.2 Best-BlastP=> >nrprot 79% Identities = 353/540 (65%), Positives = 435/540 (80%), Gaps = 1/540 (0%) emb|CAD23197.1| alkaline phosphomonoesterase [Fluoribacter gormanii] Length = 540

3535.5 Best-BlastP=> >nrprot No Hits found

3536.2 Best-BlastP=> >nrprot 58% Identities = 38/91 (41%), Positives = 58/91 (63%) ref|NP_819118.1| rhodanese domain protein [Coxiella burnetii RSA 493] gb|AAO89632.1| rhodanese domain protein [Coxiella burnetii RSA 493] Length = 124

3538.1 Best-BlastP=> >nrprot 47% Identities = 107/257 (41%), Positives = 15/257 (58%), Gaps = 2/257 (0%) ref|ZP_00025602.1| COG1052: Lactate dehydrogenase and related dehydrogenases [Ralstonia metallidurans] Length = 312

354.1 Best-BlastP=> >nrprot 67% Identities = 239/471 (50%), Positives = 320/471 (67%), Gaps = 19/471 (4%) ref|NP_820171.1| deoxyribodipyrimidine photolyase - class I [Coxiella burnetii RSA 493] Length = 472

3540.2 Best-BlastP=> >nrprot 95% Identities = 574/614 (93%), Positives = 591/614 (96%) spl|Q48806|DLPA_LEGPN Protein dlpA_pirl|S61390 dlpA protein - Legionella pneumophila gb|AAA79904.1| DlpA Length = 615

3541.1 Best-BlastP=> >nrprot 67% Identities = 127/248 (51%), Positives = 172/248 (69%), Gaps = 2/248 (0%) ref|NP_819461.1| pantotate--beta-alanine ligase [Coxiella burnetii RSA 493] gb|AAO89975.1| pantotate--beta-alanine ligase [Coxiella burnetii RSA 493] Length = 257

3542.1 Best-BlastP=> >nrprot 70% Identities = 134/256 (52%), Positives = 186/256 (72%) ref|NP_819462.1| 3-methyl-2-oxobutanoate hydroxymethyltransferase [Coxiella burnetii RSA 493] gb|AAO89976.1| 3-methyl-2-oxobutanoate hydroxymethyltransferase [Coxiella burnetii RSA 493] Length = 266

3543.1 Best-BlastP=> >nrprot 57% Identities = 87/197 (44%), Positives = 127/197 (64%) ref|NP_820749.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91263.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 205

3544.2 Best-BlastP=> >nrprot 99% Identities = 355/360 (98%), Positives = 359/360 (99%) gb|AAN17183.1|AF492466_1 hypothetical protein [Legionella pneumophila] Length = 360

3545.1 Best-BlastP=> >nrprot 64% Identities = 153/310 (49%), Positives = 211/310 (68%), Gaps = 3/310 (0%) ref|ZP_00123394.1| COG0196: FAD synthase [Haemophilus somnus 129PT] ref|ZP_00133316.1| hypothetical protein [Haemophilus somnus 2336] Length = 314

3547.1 Best-BlastP=> >nrprot 62% Identities = 64/141 (45%), Positives = 90/141 (63%), Gaps = 2/141 (1%) ref|NP_820893.1| universal stress protein A, putative [Coxiella burnetii RSA 493] sp|P45680|YJ16_COXBU Hypothetical protein CBU1916_pirl|40650 hypothetical protein 146 - Coxiella burnetii gb|AA56915.1| unknown gb|AAO91407.1| universal stress protein A, putative [Coxiella burnetii RSA 493] Length = 146

3548.2 Best-BlastP=> >nrprot 41% Identities = 104/503 (20%), Positives = 202/503 (40%), Gaps = 80/503 (15%) ref|ZP_00084271.1| COG3266: Uncharacterized protein conserved in bacteria [Pseudomonas fluorescens PfO-1] Length = 533

3550.1 Best-BlastP=> >nrprot 51% Identities = 189/192 (98%), Positives = 190/192 (98%) gb|AAF05326.1| 3-dehydroquinate synthetase homolog [Legionella pneumophila] Length = 192

3551.1 Best-BlastP=> >nrprot 75% Identities = 103/165 (62%), Positives = 133/165 (80%) ref|ZP_00134627.1| COG0703: Shikimate kinase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 173

3554.4 Best-BlastP=>>nrprot 64% Identities = 92/193 (47%), Positives = 129/193 (66%), Gaps = 5/193 (2%) refNP_794862.1| type IV pilus biogenesis protein PilO [Pseudomonas syringae pv. syringae pv. tomato str. DC3000] gb|AAO58557.1| type IV pilus biogenesis protein PilO [Pseudomonas

Length = 207

3555.2 Best-BlastP=>>nrprot 60% Identities = 72/175 (41%), Positives = 111/175 (63%) gb|AAA93087.1| membrane protein Length = 199

3556.2 Best-BlastP=>>nrprot 44% Identities = 35/118 (29%), Positives = 63/118 (53%), Gaps = 1/118 (0%) refNP_820127.1| NifU family protein [Coxiella burnetii] RSA 493] gb|AO90641.1| NifU family protein [Coxiella burnetii RSA 493] Length = 119

3557.1 Best-BlastP=>>nrprot 78% Identities = 236/383 (61%), Positives = 303/383 (79%) refNP_717860.1| cysteine desulfurase [Shewanella oneidensis MR-1] gb|AAN55304.1|AE015668_5 cysteine desulfurase [Shewanella oneidensis MR-1] Length = 404

3558.1 Best-BlastP=>>nrprot No Hits found

3559.2 Best-BlastP=>>nrprot No Hits found

3561.2 Best-BlastP=>>nrprot 99% Identities = 782/783 (99%), Positives = 783/783 (100%) pir|[T]18329 icmO protein - Legionella pneumophila [Legionella pneumophila] pir|[AAC38193.1|Dott [Legionella pneumophila] emb|[CAA75326.1| lcmO protein [Legionella pneumophila] Length = 783

3562.3 Best-BlastP=>>nrprot 99% Identities = 374/376 (99%), Positives = 376/376 (100%) pir|[T]18328 icmP protein - Legionella pneumophila [Legionella pneumophila] pir|[AAC38194.1|Dott [Legionella pneumophila] emb|[CAA75325.1| lcmP protein [Legionella pneumophila] Length = 376

3563.2 Best-BlastP=>>nrprot 47% Identities = 35/90 (38%), Positives = 55/90 (61%), Gaps = 5/90 (5%) dbj|BAC94688.1| hypothetical protein [Vibrio vulnificus YJ016] Length = 343

3564.2 Best-BlastP=>>nrprot No Hits found

3566.1 Best-BlastP=>>nrprot 76% Identities = 246/389 (63%), Positives = 305/389 (78%) refNP_716561.1| phosphoglycerate kinase [Shewanella oneidensis MR-1] sp|Q8E1B1|PGK_SHEON Phosphoglycerate kinase gb|AAN54006.1|AE015538_3 phosphoglycerate kinase [Shewanella oneidensis MR-1] Length = 391

3568.3 Best-BlastP=>>nrprot 66% Identities = 231/477 (48%), Positives = 318/477 (66%), Gaps = 6/477 (1%) refNP_743521.1| pyruvate kinase II [Pseudomonas putida KT2440] gb|AAN66985.1|AE016326_11 pyruvate kinase II [Pseudomonas putida KT2440] Length = 484

357.2 Best-BlastP=>>nrprot 75% Identities = 138/234 (58%), Positives = 177/234 (75%) refNP_540513.1| LrgB protein [Brucella melitensis] pir|[AF3451 lrgB protein [imported] - Brucella melitensis (strain 16M) gb|AAL52777.1| murein hydrolase export regulator [Brucella melitensis 16M] Length = 235

3570.2 Best-BlastP=>>nrprot 67% Identities = 33/70 (47%), Positives = 48/70 (68%) refNP_902003.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ60005.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 75

3572.1 Best-BlastP=>>nrprot 88% Identities = 109/139 (78%), Positives = 124/139 (89%) refNP_00012735.1| COG0432: Uncharacterized conserved protein [Rhodopseudomonas palustris] Length = 139

3574.1 Best-BlastP=>>nrprot 40% Identities = 83/316 (26%), Positives = 130/316 (41%), Gaps = 44/316 (13%) ref|NP_790689.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 312

3575.2 Best-BlastP=>>nrprot 42% Identities = 112/408 (27%), Positives = 192/408 (47%), Gaps = 20/408 (4%) ref|NP_638463.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42387.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 414

3578.2 Best-BlastP=>>nrprot 91% Identities = 465/524 (88%), Positives = 480/524 (91%) gb|AAC35592.1| LphB [Legionella pneumophila] Length = 518

3581.1 Best-BlastP=>>nrprot 64% Identities = 148/160 (92%), Positives = 153/160 (95%) pir|S61389 small basic protein sbpA - Legionella pneumophila gb|AAA79903.1| SbpA Length = 161

3582.2 Best-BlastP=>>nrprot 64% Identities = 134/282 (47%), Positives = 186/282 (65%), Gaps = 1/282 (0%) ref|ZP_00127817.1| hypothetical protein [Pseudomonas syringae pv. syringae B728a] Length = 288

3584.1 Best-BlastP=>>nrprot 60% Identities = 26/60 (43%), Positives = 39/60 (65%), Gaps = 2/60 (3%) ref|NP_840361.1| possible transposase [Nitrosomonas europaea ATCC 19718] ref|NP_841665.1| possible transposase [Nitrosomonas europaea ATCC 19718] Length = 135

3586.2 Best-BlastP=>>nrprot 67% Identities = 186/367 (50%), Positives = 251/367 (68%) ref|ZP_00012935.1| COG3177: Uncharacterized conserved protein [Rhodopseudomonas palustris] Length = 367

3588.2 Best-BlastP=>>nrprot 69% Identities = 83/161 (51%), Positives = 115/161 (71%) ref|NP_531634.1| methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AH2691 methyltransferase Atu0936 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAL41950.1| methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 202

359.2 Best-BlastP=>>nrprot 41% Identities = 67/120 (55%), Positives = 85/120 (70%) ref|NP_697359.1| conserved hypothetical protein [Brucella suis 1330] gb|AAN29274.1|AE014344_9 conserved hypothetical protein [Brucella suis 1330] Length = 139

3591.2 Best-BlastP=>>nrprot 65% Identities = 83/182 (45%), Positives = 124/182 (68%), Gaps = 1/182 (0%) ref|ZP_00067204.1| COG1678: Putative transcriptional regulator [Microbulbifer degradans 2-40] Length = 203

3592.1 Best-BlastP=>>nrprot 65% Identities = 73/134 (54%), Positives = 94/134 (70%) gb|AAA69116.1| ORF_0180; was also ORF_062p before splice Length = 180

3593.1 Best-BlastP=>>nrprot 62% Identities = 133/297 (44%), Positives = 193/297 (64%), Gaps = 10/297 (3%) ref|NP_821065.1| aspartate carbamoyltransferase [Coxiella burnetii RSA 493] gb|AAO91579.1| aspartate carbamoyltransferase [Coxiella burnetii RSA 493] Length = 310

3594.1 Best-BlastP=>>nrprot No Hits found

3595.1 Best-BlastP=>>nrprot 64% Identities = 39/75 (52%), Positives = 56/75 (74%) ref|NP_820996.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91510.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 81

3596.1 Best-BlastP=>>nrprot 79% Identities = 82/112 (73%), Positives = 99/112 (88%) ref|ZP_00025955.1| COG0347: Nitrogen regulatory protein PII [Ralstonia metallidurans] Length = 112

3597.3 Best-BlastP=>>nrprot 56% Identities = 73/189 (38%), Positives = 109/189 (57%), Gaps = 7/189 (3%) ref|NP_819119.1| 5-formyltetrahydrofolate cyclo-ligase family protein [Coxiella burnetii RSA 493] gb|AAO89633.1| 5-formyltetrahydrofolate cyclo-ligase family protein [Coxiella burnetii RSA 493] Length = 197

3598.3 Best-BlastP=>>nrprot No Hits found

3599.4 Best-BlastP=>>nrprot 48% Identities = 78/229 (34%), Positives = 131/229 (57%), Gaps = 3/229 (1%) ref|NP_819456.1| 4-amino-4-deoxychorismate lyase, putative [Coxiella burnetii RSA 493] gb|AAO89970.1| 4-amino-4-deoxychorismate lyase, putative [Coxiella burnetii RSA 493] Length = 281

36.1 Best-BlastP=>>nrprot 98% Identities = 606/613 (98%), Positives = 607/613 (99%) emb|CAB60062.1| lvhD4 [Legionella pneumophila] Length = 691

360.3 Best-BlastP=>>nrprot 7% Identities = 39/94 (41%), Positives = 47/94 (50%), Gaps = 1/94 (1%) ref|NP_900714.1| hypothetical protein CV1044 [Chromobacterium violaceum ATCC 12472] gb|AAQ58719.1| hypothetical protein CV1044 [Chromobacterium violaceum ATCC 12472] Length = 499

3600.2 Best-BlastP=>>nrprot 66% Identities = 147/311 (47%), Positives = 207/311 (66%), Gaps = 1/311 (0%) ref|NP_232559.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|H82491 conserved hypothetical protein VCA0159 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF96072.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 313

3601.1 Best-BlastP=>>nrprot 68% Identities = 183/385 (47%), Positives = 262/385 (68%), Gaps = 8/385 (2%) ref|ZP_00065865.1| COG3004: Na+/H+ antiporter [Microbulbifer degradans 2-40] Length = 401

3602.2 Best-BlastP=>>nrprot 20% Identities = 73/282 (25%), Positives = 120/282 (42%), Gaps = 50/282 (17%) gb|IEAA19568.1| hypothetical protein [Plasmoidium yoelii yoelii] Length = 5074

3607.2 Best-BlastP=>>nrprot 56% Identities = 158/379 (41%), Positives = 224/379 (59%), Gaps = 12/379 (3%) ref|ZP_00128328.1| COG2850: Uncharacterized conserved protein [Pseudomonas syringae pv. syringae B728a] Length = 388

3608.1 Best-BlastP=>>nrprot No Hits found

3609.1 Best-BlastP=>>nrprot 99% Identities = 191/192 (99%), Positives = 192/192 (100%) sp|P31108|SODF_LEGPN Superoxide dismutase [Fe] pir|JS0749 superoxide dismutase (EC 1.15.1.1) (Fe) - Legionella pneumophila dbj|BA02306.1| iron superoxide dismutase (Fe-SOD) [Legionella pneumophila] gb|AAM00603.1| superoxide dismutase [Legionella pneumophila] prf|2014300A Fe superoxide dismutase Length = 192

3610.1 Best-BlastP=>>nrprot 72% Identities = 202/384 (52%), Positives = 284/384 (73%) ref|NP_841480.1| argD; acetylornithine aminotransferase [Nitrosomonas europaea ATCC 19718] emb|CAD85350.1| argD; acetylornithine aminotransferase [Nitrosomonas europaea ATCC 19718] Length = 393

3611.2 Best-BlastP=>>nrprot 66% Identities = 119/254 (46%), Positives = 169/254 (66%), Gaps = 2/254 (0%) ref|NP_440288.1| unknown protein [Synechocystis sp. PCC 6803] pir|S74928 hypothetical protein sll0647 - Synechocystis sp. (strain PCC 6803) dbj|BA16968.1| ORF_ID sll0647~unknown protein [Synechocystis sp. PCC 6803] Length = 256

3612.2 Best-BlastP=>>nrprot 40% Identities = 68/222 (30%), Positives = 106/222 (47%), Gaps = 16/222 (7%) ref|NP_229421.1| hypothetical protein [Thermotoga maritima] pir|G72232 hypothetical protein - Thermotoga maritima (strain MSB8) gb|AAD3668.1|AE001805_13 hypothetical protein [Thermotoga maritima] Length = 222

3613.3 Best-BlastP=>>nprot 75% Identities = 245/422 (58%), Positives = 326/422 (77%), Gaps = 2/422 (0%) ref|NP_405097.1| NAD-dependent malic enzyme [Yersinia pestis] ref|NP_669960.1| NAD-linked malate dehydrogenase (malic enzyme) [Yersinia pestis] KIM pir|AC0184 malate dehydrogenase (oxaloacetate-decarboxylating) (EC 1.1.1.38) [imported] - Yersinia pestis (strain CO92) embl|CAC90334.1| NAD-dependent malic enzyme [Yersinia pestis CO92] gb|AAM86211.1|AE013868_5 NAD-linked malate dehydrogenase (malic enzyme) [Yersinia pestis] KIM] Length = 565

3614.3 Best-BlastP=>>nprot 99% Identities = 353/354 (99%), Positives = 354/354 (100%) gb|AAM00637.1| putative cobalt/magnesium uptake transporter [Legionella pneumophila] Length = 354

3617.2 Best-BlastP=>>nprot 83% Identities = 68/101 (67%), Positives = 85/101 (84%) ref|NP_820421.1| NADH dehydrogenase I, K subunit [Coxiella burnetii RSA 493] gb|AAO90935.1| NADH dehydrogenase I, K subunit [Coxiella burnetii RSA 493] Length = 101

3618.2 Best-BlastP=>>nprot 72% Identities = 388/654 (59%), Positives = 480/654 (73%), Gaps = 4/654 (0%) ref|NP_820420.1| NADH dehydrogenase I, L subunit [Coxiella burnetii RSA 493] gb|AAO90934.1| NADH dehydrogenase I, L subunit [Coxiella burnetii RSA 493] Length = 653

3619.1 Best-BlastP=>>nprot 70% Identities = 63/137 (45%), Positives = 100/137 (72%) ref|NP_253434.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9HV53|YBE6_PSEAE Hypothetical UPF0090 protein PA4746 pir|A83053 conserved hypothetical protein PA4746 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08132.1|AE004888_7 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 152

3621.2 Best-BlastP=>>nprot 78% Identities = 307/491 (62%), Positives = 385/491 (78%), Gaps = 2/491 (0%) ref|ZP_00066603.1| COG0195: Transcription elongation factor [Microbulbifer degradans 2-40] Length = 493

3622.3 Best-BlastP=>>nprot 71% Identities = 168/313 (53%), Positives = 226/313 (72%), Gaps = 1/313 (0%) ref|ZP_00092328.1| hypothetical protein [Azotobacter vinelandii] Length = 379

3623.2 Best-BlastP=>>nprot 73% Identities = 74/123 (60%), Positives = 92/123 (74%), Gaps = 1/123 (0%) ref|NP_716411.1| glycine cleavage system H protein [Shewanella oneidensis MR-1] Length = 129

3625.2 Best-BlastP=>>nprot 73% Identities = 270/452 (59%), Positives = 338/452 (74%), Gaps = 2/452 (0%) ref|NP_840693.1| Glycine cleavage system P-protein [Nitrosomonas europaea ATCC 19718] Length = 453

3626.1 Best-BlastP=>>nprot 59% Identities = 44/90 (48%), Positives = 61/90 (67%) ref|NP_713147.1| conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb|AAN53856.1|AE015522_11 glycine cleavage system H protein [Shewanella oneidensis MR-1] Length = 104

3629.2 Best-BlastP=>>nprot 75% Identities = 170/291 (58%), Positives = 223/291 (76%) ref|ZP_00065024.1| COG1159: GTPase [Microbulbifer degradans 2-40] Length = 298

3631.4 Best-BlastP=>>nprot No Hits found

3632.3 Best-BlastP=>>nprot 49% Identities = 273/1022 (26%), Positives = 507/1022 (49%), Gaps = 42/1022 (4%) gb|AAP44228.1| transposase TnpA [Pseudomonas sp. ND6] Length = 1009

3633.3 Best-BlastP=>>nprot 63% Identities = 122/307 (39%), Positives = 196/307 (63%) ref|NP_819755.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90269.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 308

3634.1 Best-BlastP=>>nrprot 55% Identities = 103/103 (100%), Positives = 103/103 (100%) ref|P26880|YPA1_LEGPN Hypothetical protein in PAL 5'region (ORFU) Length = 103

3636.1 Best-BlastP=>>nrprot 99% Identities = 176/176 (100%), Positives = 176/176 (100%) ref|P26493|PAL_LEGPN Peptidoglycan-associated lipoprotein precursor (19 kDa surface antigen) (PPL) pir|A60337 outer membrane protein ppa, peptidoglycan-associated, precursor - Legionella pneumophila emb|CAA43033.1| lipoprotein antigen [Legionella pneumophila] Length = 176

3637.1 Best-BlastP=>>nrprot 59% Identities = 188/201 (93%), Positives = 193/201 (96%), Gaps = 4/201 (1%) ref|P26881|YPA2_LEGPN Hypothetical protein in PAL 3'region (ORFD) Length = 201

3638.2 Best-BlastP=>>nrprot 78% Identities = 141/217 (64%), Positives = 171/217 (78%), Gaps = 1/217 (0%) ref|ZP_00083811.1| COG0602: Organic radical activating enzymes [Pseudomonas fluorescens PfO-1] Length = 218

364.2 Best-BlastP=>>nrprot 5% Identities = 31/70 (44%), Positives = 38/70 (54%), Gaps = 3/70 (4%) ref|NP_900714.1| hypothetical protein CV1044 [Chromobacterium violaceum ATCC 12472] gb|AAQ58719.1| hypothetical protein CV1044 [Chromobacterium violaceum ATCC 12472] Length = 499

3640.2 Best-BlastP=>>nrprot 51% Identities = 94/313 (30%), Positives = 162/313 (51%), Gaps = 21/313 (6%) ref|CAC51371.1| mevalonate diphosphate decarboxylase [Lactobacillus helveticus] Length = 320

3641.1 Best-BlastP=>>nrprot 42% Identities = 65/228 (28%), Positives = 108/228 (47%), Gaps = 12/228 (5%) ref|NP_820494.1| transporter, ZTP family [Coxiella burnetii RSA 493] gb|AAO91008.1| transporter, ZTP family [Coxiella burnetii RSA 493] Length = 261

3642.2 Best-BlastP=>>nrprot 57% Identities = 154/329 (46%), Positives = 220/329 (66%), Gaps = 3/329 (0%) ref|NP_820351.1| cation-efflux family protein [Coxiella burnetii RSA 493] gb|AAO90865.1| cation-efflux family protein [Coxiella burnetii RSA 493] Length = 378

3645.3 Best-BlastP=>>nrprot 67% Identities = 132/255 (51%), Positives = 171/255 (67%), Gaps = 15/255 (5%) ref|ZP_00016164.1| COG0378: Ni2+-binding GTPase involved in regulation of expression Length = 268

3647.2 Best-BlastP=>>nrprot 71% Identities = 37/67 (55%), Positives = 54/67 (80%) ref|ZP_00021586.1| COG0298: Hydrogenase maturation factor [Ralstonia metallidurans] Length = 103

365.4 Best-BlastP=>>nrprot 49% Identities = 88/327 (26%), Positives = 165/327 (50%), Gaps = 15/327 (4%) ref|NP_819818.1| multidrug resistance protein [Coxiella burnetii RSA 493] gb|AAO90332.1| multidrug resistance protein [Coxiella burnetii RSA 493] Length = 331

3650.1 Best-BlastP=>>nrprot 52% Identities = 171/363 (47%), Positives = 221/363 (60%), Gaps = 8/363 (2%) ref|ZP_00089787.1| COG1145: Ferredoxin [Azotobacter vinelandii] Length = 382

3651.1 Best-BlastP=>>nrprot 56% Identities = 114/269 (42%), Positives = 158/269 (58%), Gaps = 3/269 (1%) ref|ZP_00089785.1| COG0543: 2- polyphenylphenol hydroxylase and related flavodoxin oxidoreductases [Azotobacter vinelandii] Length = 283

3652.2 Best-BlastP=>>nrprot 64% Identities = 132/249 (53%), Positives = 169/249 (67%), Gaps = 1/249 (0%) ref|ZP_00089784.1| COG1941: Coenzyme F420-reducing hydrogenase, gamma subunit [Azotobacter vinelandii] Length = 256

3653.3 Best-BlastP=>>nrprot 56% Identities = 26/40 (65%), Positives = 33/40 (82%), Gaps = 3/40 (7%) gb|AAG45149.1| TraA-like protein [Legionella pneumophila] Length = 883

3655.1 Best-BlastP=>>nrprot No Hits found

3657.1 Best-BlastP=>>nrprot 48% Identities = 65/171 (38%), Positives = 103/171 (60%), Gaps = 2/171 (1%) ref|NP_174343.2| expressed protein [Arabidopsis thaliana] Length = 391

3658.1 Best-BlastP=>>nrprot No Hits found

3659.2 Best-BlastP=>>nrprot No Hits found

366.2 Best-BlastP=>>nrprot No Hits found

3661.4 Best-BlastP=>>nrprot 32% Identities = 71/191 (37%), Positives = 108/191 (56%), Gaps = 22/191 (11%) ref|NP_901795.1| hypothetical protein CV2125 [Chromobacterium violaceum ATCC 12472] Length = 202

3663.1 Best-BlastP=>>nrprot No Hits found

3664.1 Best-BlastP=>>nrprot 52% Identities = 142/332 (42%), Positives = 203/332 (61%), Gaps = 5/332 (1%) gbl|AAK49795.1| WcbbB [Burkholderia pseudomallei] Length = 365

3665.1 Best-BlastP=>>nrprot 52% Identities = 109/243 (44%), Positives = 162/243 (66%) ref|ZP_00125435.1| COG0500: SAM-dependent methyltransferases [Pseudomonas syringae pv. syringae B728a] Length = 646

3666.2 Best-BlastP=>>nrprot 44% Identities = 121/287 (42%), Positives = 173/287 (60%), Gaps = 2/287 (0%) gbl|AAK49795.1| WcbbB [Burkholderia pseudomallei] Length = 365

3667.1 Best-BlastP=>>nrprot No Hits found

3669.1 Best-BlastP=>>nrprot 83% Identities = 227/316 (71%), Positives = 264/316 (83%) ref|NP_820997.1| cystathione beta-synthase, putative [Coxiella burnetii RSA 493] gbl|AAO91511.1| cystathione beta-synthase, putative [Coxiella burnetii RSA 493] Length = 316

3670.2 Best-BlastP=>>nrprot No Hits found

3671.2 Best-BlastP=>>nrprot 24% Identities = 34/134 (25%), Positives = 59/134 (44%), Gaps = 7/134 (5%) ref|XP_283791.1| RIKEN cDNA B230210E21 gene [Mus musculus] Length = 484

3673.2 Best-BlastP=>>nrprot 51% Identities = 137/403 (33%), Positives = 211/403 (52%), Gaps = 9/403 (2%) ref|NP_793575.1| major facilitator family transporter [Pseudomonas syringae pv. tomato str. DC3000] gbl|AO057270.1| major facilitator family transporter [Pseudomonas syringae pv. tomato str. DC3000] Length = 445

3674.2 Best-BlastP=>>nrprot 63% Identities = 123/273 (45%), Positives = 173/273 (63%), Gaps = 17/273 (6%) ref|ZP_00084952.1| COG1766: Flagellar biosynthesis/type III secretory pathway lipoprotein [Pseudomonas fluorescens PfO-1] Length = 595

3675.1 Best-BlastP=>>nrprot 60% Identities = 45/87 (51%), Positives = 64/87 (73%), Gaps = 5/87 (5%) dbj|BAC95246.1| flagellar hook-basal body protein FlIE [Vibrio vulnificus YJ016] Length = 122

3676.2 Best-BlastP=>>nrprot 60% Identities = 261/267 (97%), Positives = 263/267 (98%) gbl|AAG45148.1| putative response regulator [Legionella pneumophila] Length = 267

3679.3 Best-BlastP=>>nrprot 56% Identities = 129/324 (39%), Positives = 194/324 (59%), Gaps = 5/324 (1%) ref|NP_746486.1| sensory box histidine kinase FlsS [Pseudomonas putida KT2440] Length = 405

368.2 Best-BlastP=>>nrprot 22% Identities = 123/487 (25%), Positives = 188/487 (38%), Gaps = 62/487 (12%) emb|CAD27470.1| SPAPB18E9.04c [Schizosaccharomyces pombe] Length = 800

3680.1 Best-BlastP=>>nrprot 84% Identities = 230/314 (73%), Positives = 268/314 (85%) ref|ZP_00135925.1| COG0492: Thioredoxin reductase
[Pseudomonas aeruginosa UCBPP-PA14] Length = 316

3681.1 Best-BlastP=>>nrprot 63% Identities = 110/221 (49%), Positives = 142/221 (64%), Gaps = 3/221 (1%) ref|NP_842221.1| Leucyl/phenylalanyl-tRNA-protein transferase [Nitrosomonas europaea ATCC 19718] sp|Q82ST5|LFFTR_NITEU Leucyl/phenylalanyl-tRNA-protein transferase (L/F-transferase) (Leucyltransferase) (Phenylalanyltransferase) (Leucyl/phenylalanyl-tRNA-protein transferase [Nitrosomonas europaea ATCC 19718] Length = 236

3682.1 Best-BlastP=>>nrprot 66% Identities = 58/122 (47%), Positives = 83/122 (68%) ref|NP_819118.1| rhodanese domain protein [Coxiella burnetii RSA 493] gb|AAO89632.1| rhodanese domain protein [Coxiella burnetii RSA 493] Length = 124

3683.2 Best-BlastP=>>nrprot 93% Identities = 63/72 (87%), Positives = 69/72 (95%) ref|NP_404963.1| translation initiation factor IF-1 [Yersinia pestis] ref|NP_670107.1| protein chain initiation factor IF-1 [Yersinia pestis KIM] ref|NP_928886.1| translation initiation factor IF-1 [Photorhabdus luminescens subsp. laumondii TTO1] sp|Q8ZGD3|IF1 YERPE Translation initiation factor IF-1_1 pir|AD0167 translation initiation factor IF-1 [Imported] - Yersinia pestis (strain CO92) emb|CAC90199.1| translation initiation factor IF-1 [Yersinia pestis CO92] gb|AM86358.1|AE013884_5 protein chain initiation factor IF-1 [Yersinia pestis KIM] emb|CAE13888.1| translation initiation factor IF-1 [Photorhabdus luminescens subsp. laumondii TTO1] Length = 72

3684.2 Best-BlastP=>>nrprot 30% Identities = 27/117 (23%), Positives = 61/117 (52%), Gaps = 2/117 (1%) ref|NP_716604.1| hypothetical protein [Shewanella oneidensis MR-1] gb|AN54049.1|AE015542_5 hypothetical protein [Shewanella oneidensis MR-1] Length = 474

3685.1 Best-BlastP=>>nrprot 47% Identities = 41/88 (46%), Positives = 52/88 (59%), Gaps = 2/88 (2%) ref|NP_800276.1| putative glutamate synthetase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62109.1| putative glutamate synthetase [Vibrio parahaemolyticus] Length = 513

3686.1 Best-BlastP=>>nrprot 39% Identities = 118/353 (33%), Positives = 206/353 (58%), Gaps = 1/353 (0%) ref|ZP_00084494.1| COG2199: FOG: GGDEF domain [Pseudomonas fluorescens PFO-1] Length = 696

3687.1 Best-BlastP=>>nrprot 70% Identities = 182/294 (61%), Positives = 232/294 (78%) ref|NP_294489.1| lipoic acid synthase [Deinococcus radiodurans] sp|Q9RWA4|LIPA_DERIA Lipoic acid synthetase (Lip-syn) (Lipoate synthase) pir|A75480 lipoic acid synthase - Deinococcus radiodurans (strain R1) gb|AAF10341.1|AE001931_12 lipoic acid synthase [Deinococcus radiodurans] Length = 331

3688.1 Best-BlastP=>>nrprot 59% Identities = 42/90 (46%), Positives = 56/90 (62%), Gaps = 2/90 (2%) ref|NP_773278.1| blr6638 [Bradyrhizobium japonicum] dbj|BAC51903.1| blr6638 [Bradyrhizobium japonicum USDA 110] Length = 112

3694.2 Best-BlastP=>>nrprot 81% Identities = 246/361 (68%), Positives = 294/361 (81%) ref|NP_819175.1| phospho-N-acetylumuramoyl-pentapeptide-transferase [Coxiella burnetii RSA 493] Length = 361

3697.4 Best-BlastP=>>nrprot 61% Identities = 456/1174 (38%), Positives = 715/1174 (60%), Gaps = 26/1174 (2%) ref|ZP_00065347.1| COG1196: Chromosome segregation ATPases [Microbulbifer degradans] 2-40] Length = 1168

3699.3 Best-BlastP=>>nrprot No Hits found

37.1 Best-BlastP=>>nrprot 98% Identities = 322/334 (96%), Positives = 330/334 (98%) gb|IAAM08248.1| putative component of the type IV secretion system [Legionella pneumophila] Length = 334

3701.1 Best-BlastP=> >nrprot 31% Identities = 57/156 (36%), Positives = 84/156 (53%), Gaps = 8/156 (5%) ref|NP_522544.1| PROBABLE TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum] Length = 227

3702.1 Best-BlastP=> >nrprot 69% Identities = 131/242 (54%), Positives = 172/242 (71%), Gaps = 4/242 (1%) ref|NP_284288.1| putative pseudouridine synthase [Neisseria meningitidis Z2491] pir|H81849 probable pseudouridine synthase NMA1573 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB84800.1| putative pseudouridine synthase [Neisseria meningitidis Z2491] Length = 256

3703.1 Best-BlastP=> >nrprot 67% Identities = 90/173 (52%), Positives = 130/173 (75%) ref|ZP_00127917.1| COG1386: Predicted transcriptional regulator containing the HTH domain [Pseudomonas syringae pv. syringae B728a] Length = 255

3705.1 Best-BlastP=> >nrprot 70% Identities = 140/250 (56%), Positives = 186/250 (74%) ref|NP_642633.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri] str. 306] Length = 279

3706.2 Best-BlastP=> >nrprot 77% Identities = 254/396 (64%), Positives = 314/396 (79%) ref|NP_519264.1| PROBABLE TRYPTOPHANYL-tRNA SYNTETASE (SYW PROTEIN) [Ralstonia solanacearum] sp|Q8Y0A1|SYW_RALSO Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS) emb|CAD14845.1| PROBABLE TRYPTOPHANYL-tRNA SYNTETASE (SYW PROTEIN) [Ralstonia solanacearum] Length = 400

3708.1 Best-BlastP=> >nrprot 75% Identities = 130/205 (63%), Positives = 167/205 (81%) ref|ZP_00067787.1| COG0009: Putative translation factor (SUA5) [Microbulbifer degradans 2-40] Length = 207

3709.1 Best-BlastP=> >nrprot 58% Identities = 119/275 (43%), Positives = 165/275 (60%), Gaps = 2/275 (0%) ref|NP_841756.1| PHP domain N-terminal region:PHP domain C-terminal region [Nitrosomonas europaea ATCC 19718] emb|CAD85635.1| PHP domain N-terminal region:PHP domain C-terminal region [Nitrosomonas europaea ATCC 19718] Length = 316

3710.1 Best-BlastP=> >nrprot 67% Identities = 152/329 (46%), Positives = 214/329 (65%), Gaps = 25/329 (7%) ref|NP_245983.1| PhoH [Pasteurella multocida] gb|AAK03130.1| PhoH [Pasteurella multocida] Length = 372

3711.1 Best-BlastP=> >nrprot 66% Identities = 78/152 (51%), Positives = 105/152 (69%), Gaps = 2/152 (1%) ref|NP_746893.1| conserved hypothetical protein TIGR00043 [Pseudomonas putida KT2440] gb|AAN70357.1|AE016677_8 conserved hypothetical protein TIGR00043 [Pseudomonas putida KT2440] Length = 157

3712.2 Best-BlastP=> >nrprot 65% Identities = 139/261 (53%), Positives = 189/261 (72%) dbl|BAC93678.1| putative hemolysin [Vibrio vulnificus YJ016] Length = 306

3714.3 Best-BlastP=> >nrprot No Hits found

3720.2 Best-BlastP=> >nrprot 86% Identities = 192/264 (72%), Positives = 228/264 (86%) ref|ZP_00024661.1| COG0207: Thymidylate synthase [Ralstonia metallidurans] Length = 264

3721.1 Best-BlastP=> >nrprot 64% Identities = 79/143 (55%), Positives = 101/143 (70%) ref|NP_819678.1| riboflavin synthase, beta subunit [Coxiella burnetii RSA 493] gb|AAO90192.1| riboflavin synthase, beta subunit [Coxiella burnetii RSA 493] Length = 151

3729.1 Best-BlastP=>>nrprot 53% Identities = 70/188 (37%), Positives = 101/188 (53%), Gaps = 14/188 (7%) ref|NP_636438.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM40362.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 176

3730.1 Best-BlastP=>>nrprot No Hits found

3731.1 Best-BlastP=>>nrprot 63% Identities = 56/114 (49%), Positives = 77/114 (67%), Gaps = 1/114 (0%) ref|NP_890078.1| phage integrase [Bordetella bronchiseptica] emb|CAE34037.1| phage integrase [Bordetella bronchiseptica] Length = 407

3732.1 Best-BlastP=>>nrprot 36% Identities = 58/180 (32%), Positives = 107/180 (59%), Gaps = 1/180 (0%) ref|NP_624053.1| predicted transposase [Thermoanaerobacter tengcongensis] gb|AAM25657.1| predicted transposase [Thermoanaerobacter tengcongensis] Length = 267

3734.1 Best-BlastP=>>nrprot 37% Identities = 86/323 (26%), Positives = 140/323 (43%), Gaps = 53/323 (16%) ref|NP_563745.1| expressed protein [Arabidopsis thaliana] gb|AAM65464.1| unknown [Arabidopsis thaliana] gb|AAN72060.1| expressed protein [Arabidopsis thaliana] gb|AAP42733.1| At1g05620 [Arabidopsis thaliana] Length = 322

3735.2 Best-BlastP=>>nrprot 36% Identities = 106/496 (21%), Positives = 199/496 (40%), Gaps = 61/496 (12%) gb|EAA16521.1| 235 kDa rhoptry protein [Plasmodium yoelii yoelii] Length = 2740

3737.1 Best-BlastP=>>nrprot No Hits found

3739.3 Best-BlastP=>>nrprot 79% Identities = 100/146 (68%), Positives = 117/146 (80%) ref|NP_539647.1| LACTOYL GLUTATHIONE LYASE [Brucella melitensis] pir|AD3343 lactoylglutathione lyase (EC 4.4.1.5) [Imported] - Brucella melitensis (strain 16M) gb|AAL51911.1| LACTOYL GLUTATHIONE LYASE [Brucella melitensis 16M] Length = 173

3742.2 Best-BlastP=>>nrprot 66% Identities = 302/595 (50%), Positives = 393/595 (66%), Gaps = 13/595 (2%) ref|ZP_00029131.1| COG3243: Poly(3-hydroxyalkanoate) synthetase [Burkholderia fungorum] Length = 642

3740.3 Best-BlastP=>>nrprot 72% Identities = 95/159 (59%), Positives = 128/159 (80%) ref|ZP_00021733.1| COG2862: Predicted membrane protein [Ralstonia metallidurans] Length = 206

3741.1 Best-BlastP=>>nrprot 32% Identities = 61/271 (22%), Positives = 133/271 (49%), Gaps = 18/271 (6%) ref|XP_230851.2| similar to hypothetical protein [Rattus norvegicus] Length = 396

3742.1 Best-BlastP=>>nrprot No Hits found

3743.1 Best-BlastP=>>nrprot No Hits found

3744.2 Best-BlastP=>>nrprot No Hits found

3747.2 Best-BlastP=>>nrprot 49% Identities = 99/264 (37%), Positives = 149/264 (56%), Gaps = 7/264 (2%) ref|NP_743187.1| peptidase, M23/M37 family [Pseudomonas putida KT2440] gb|AAN66651.1|AE016293_1 peptide, M23/M37 family [Pseudomonas putida KT2440] Length = 275

3748.1 Best-BlastP=>>nrprot 63% Identities = 192/445 (43%), Positives = 280/445 (62%), Gaps = 5/445 (1%) ref|NP_461447.1| exonuclease VII, large subunit [Salmonella typhimurium LT2] sp|Q8ZN58|EX7L_SALTY Probable exodeoxyribonuclease VII large subunit (Exonuclease VII subunit) gb|AAL21406.1| exonuclease VII, large subunit [Salmonella typhimurium LT2] Length = 449

3750.2 Best-BlastP=>>nrprot 42% Identities = 156/424 (36%), Positives = 245/424 (57%), Gaps = 2/424 (0%) prl|S27611 agglutination protein - Pseudomonas putida gb|AAA25695.1| agglutination protein Length = 452

3752.2 Best-BlastP=> >nrprot 54% Identities = 82/187 (43%), Positives = 116/187 (62%), Gaps = 2/187 (1%) ref|ZP_00065146.1| COG3672: Predicted periplasmic protein [Microbulbifer degradans 2-40] Length = 241

3753.2 Best-BlastP=> >nrprot 55% Identities = 197/655 (30%), Positives = 352/655 (53%), Gaps = 41/655 (6%) ref|ZP_00086698.1| COG2200: FOG: EAL domain [Pseudomonas fluorescens PfO-1] Length = 648

3754.2 Best-BlastP=> >nrprot 36% Identities = 48/170 (28%), Positives = 88/170 (51%), Gaps = 11/170 (6%) ref|NP_773217.1| bll6577 [Bradyrhizobium japonicum] dbj|BAC51842.1| bll6577 [Bradyrhizobium japonicum USDA 110] Length = 237

3756.2 Best-BlastP=> >nrprot 67% Identities = 234/439 (53%), Positives = 301/439 (68%), Gaps = 7/439 (1%) ref|NP_713336.1| putative flavin-containing monooxygenase [Leptospira interrogans serovar lai str. 56601] gb|AN50354.1|AE011478_5 putative flavin-containing monooxygenase [Leptospira interrogans serovar lai str. 56601] Length = 468

376.3 Best-BlastP=> >nrprot 69% Identities = 155/329 (47%), Positives = 230/329 (69%), Gaps = 4/329 (1%) ref|NP_931992.1| glycerol-3-phosphate dehydrogenase [NAD(P)H-dependent laumondii TTO1] emb|CAE17210.1| glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H)-dependent luminescens subsp. laumondii TTO1] Length = 340

3760.3 Best-BlastP=> >nrprot 69% Identities = 292/614 (47%), Positives = 418/614 (68%), Gaps = 13/614 (2%) ref|NP_924289.1| glutathione-regulated potassium efflux system protein KefC homolog [Gloeobacter violaceus] dbj|BAC89284.1| gtr1343 [Gloeobacter violaceus] Length = 634

3761.1 Best-BlastP=> >nrprot No Hits found

3763.1 Best-BlastP=> >nrprot 44% Identities = 59/195 (30%), Positives = 90/195 (46%), Gaps = 34/195 (17%) ref|NP_052362.1| unnamed protein product [Coxiella burnetii] ref|NP_819025.1| hypothetical protein [Coxiella burnetii RSA 493] pir|S38244 hypothetical protein - Coxiella burnetii emb|CAA53132.1| unnamed protein product [Coxiella burnetii] gb|AO91585.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 361

3764.3 Best-BlastP=> >nrprot No Hits found

3765.1 Best-BlastP=> >nrprot 46% Identities = 80/315 (25%), Positives = 147/315 (46%), Gaps = 20/315 (6%) ref|ZP_00124222.1| COG1721: Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) [Pseudomonas syringae pv. syringae B728a] Length = 327

377.1 Best-BlastP=> >nrprot 66% Identities = 137/265 (51%), Positives = 185/265 (69%), Gaps = 6/265 (2%) ref|NP_819341.1| glutamate racemase [Coxiella burnetii RSA 493] gb|AO898955.1| glutamate racemase [Coxiella burnetii RSA 493] Length = 280

3771.2 Best-BlastP=> >nrprot 66% Identities = 105/197 (53%), Positives = 138/197 (70%), Gaps = 2/197 (1%) ref|NP_717670.1| phosphoribosyl-ATP pyrophosphatase/phosphoribosyl-AMP cyclohydrolase [Shewanella oneidensis MR-1] gb|AN55114.1|AE015648_7 phosphoribosyl-ATP pyrophosphatase/phosphoribosyl-AMP cyclohydrolase [Shewanella oneidensis MR-1] Length = 211

3772.2 Best-BlastP=>>nrprot 69% Identities = 185/353 (52%), Positives = 245/353 (69%), Gaps = 2/353 (0%) ref|NP_405132.1| histidinol-phosphatase and imidazoleglycerol-phosphate dehydratase [Yersinia pestis] ref|NP_669926.1| imidazoleglycerolphosphate dehydratase; histidinol-phosphate phosphatase [Yersinia pestis KIM] sp|Q8ZFX7|HIS7 YERP Histidine biosynthesis bifunctional protein hisB [Includes: Histidinol-phosphatase ; Imidazoleglycerol-phosphate dehydratase (IGPD) pir|AF0188 imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) [imported] - Yersinia pestis (strain CO92) emb|CAC90369.1| histidinol-phosphatase and imidazoleglycerol-phosphate dehydratase [Yersinia pestis CO92] gb|AAM86177.1|AE013864_4 imidazoleglycerolphosphate dehydratase; histidinol-phosphate phosphatase [Yersinia pestis KIM] Length = 355

3778.2 Best-BlastP=>>nrprot 62% Identities = 50/84 (59%), Positives = 62/84 (73%) ref|ZP_00038938.1| COG4496: Uncharacterized protein conserved in bacteria [Xylella fastidiosa Dixon] Length = 112

3780.2 Best-BlastP=>>nrprot 23% Identities = 30/60 (50%), Positives = 37/60 (61%), Gaps = 5/60 (8%) ref|NP_700818.1| merozoite surface protein 3 [Plasmodium falciparum 3D7] gb|AAC09377.1| antigen [Plasmodium falciparum] gb|AAN35542.1|AE014834_39 merozoite surface protein 3 [Plasmodium falciparum 3D7] Length = 354

3783.1 Best-BlastP=>>nrprot 75% Identities = 55/95 (57%), Positives = 74/95 (77%) ref|ZP_00096296.1| COG2827: Predicted endonuclease containing a URI domain [Novosphingobium aromaticivorans] Length = 111

3784.2 Best-BlastP=>>nrprot 72% Identities = 190/364 (52%), Positives = 266/364 (73%), Gaps = 3/364 (0%) ref|ZP_00122463.1| COG3842: ABC-type spermidine/putrescine transport systems, ATPase components [Haemophilus somnus 129PT] Length = 372

3785.2 Best-BlastP=>>nrprot 71% Identities = 124/276 (44%), Positives = 203/276 (73%), Gaps = 2/276 (0%) ref|NP_439497.1| spermidine/putrescine ABC transporter permease protein [Haemophilus influenzae Rd] sp|P45170|POTB_HAEIN Spermidine/putrescine transport system permease potB - Haemophilus influenzae (strain Rd KW20) gbi|AAC22990.1| spermidine/putrescine ABC transporter, permease protein (potB) [Haemophilus influenzae Rd] Length = 286

3788.1 Best-BlastP=>>nrprot 68% Identities = 115/251 (45%), Positives = 176/251 (70%) ref|ZP_00128580.1| COG1177: ABC-type spermidine/putrescine transport system, permease component II [Desulfovibrio desulfuricans G20] Length = 257

3789.2 Best-BlastP=>>nrprot 65% Identities = 122/283 (43%), Positives = 187/283 (66%), Gaps = 3/283 (1%) ref|NP_231067.1| spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82201 (strain N16961 serogroup O1) gb|AAF94581.1| spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 345

3791.1 Best-BlastP=>>nrprot No Hits found

3792.1 Best-BlastP=>>nrprot No Hits found

3793.3 Best-BlastP=>>nrprot 43% Identities = 78/264 (29%), Positives = 132/264 (50%), Gaps = 10/264 (3%) ref|ZP_00018971.1| hypothetical protein [Chloroflexus aurantiacus] Length = 303

3796.3 Best-BlastP=>>nrprot 58% Identities = 87/178 (48%), Positives = 120/178 (67%) ref|NP_840387.1| Bacterial regulatory proteins, TetR family [Nitrosomonas europaea ATCC 19718] Length = 213

3797.1 Best-BlastP=>>nrprot 68% Identities = 167/346 (48%), Positives = 239/346 (69%), Gaps = 6/346 (1%) ref|NP_831149.1| Nitropropane dioxygenase / Trans-enoyl-CoA reductase family [Bacillus cereus ATCC 14579] gb|AAP08350.1| Nitropropane dioxygenase / Trans-enoyl-CoA reductase family [Bacillus cereus ATCC 14579] Length = 363

3798.1 Best-BlastP=>>nrprot No Hits found

3800.4 Best-BlastP=>>nrprot No Hits found

3801.2 Best-BlastP=>>nrprot 99% Identities = 477/483 (98%), Positives = 481/483 (99%) gb|AAM00644.1| adenylylate cyclase [Legionella pneumophila] Length = 483

3802.2 Best-BlastP=>>nrprot 63% Identities = 189/413 (45%), Positives = 270/413 (65%), Gaps = 2/413 (0%) ref|NP_742893.1| glutamyl-tRNA reductase [Pseudomonas putida KT2440] gb|AAN66357.1|AE016264_1 glutamyl-tRNA reductase [Pseudomonas putida KT2440] Length = 425

3803.1 Best-BlastP=>>nrprot 84% Identities = 235/358 (65%), Positives = 306/358 (85%) ref|NP_820940.1| peptide chain release factor 1 [Coxiella burnetii RSA 493] sp|P47849|RF1_COXBU Peptide chain release factor 1 (RF-1) gb|AAO91454.1| peptide chain release factor 1 [Coxiella burnetii RSA 493] Length = 361

3804.2 Best-BlastP=>>nrprot 66% Identities = 134/281 (47%), Positives = 192/281 (68%), Gaps = 6/281 (2%) ref|ZP_00066170.1| COG2890: Methylase of polypeptide chain release factors [Microbulbifer degradans 2-40] Length = 288

3807.2 Best-BlastP=>>nrprot 84% Identities = 97/133 (72%), Positives = 115/133 (86%) ref|NP_706093.1| dnaK suppressor protein [Shigella flexneri 2a str. 301] ref|NP_752128.1| DnaK suppressor protein [Escherichia coli CFT073] gb|AAN41800.1|AE015050_16 dnaK suppressor protein [Shigella flexneri 2a str. 301] gb|AAN78672.1|AE016755_172 DnaK suppressor protein [Escherichia coli CFT073] Length = 157

381.6 Best-BlastP=>>nrprot 24% Identities = 141/721 (19%), Positives = 282/721 (39%), Gaps = 94/721 (13%) ref|NP_010225.1| involved intracellular protein transport, coiled-coil protein necessary for protein transport from ER to Golgi; Usolp [Saccharomyces cerevisiae] pirl|S67593 transport protein USO1 - yeast (Saccharomyces cerevisiae) emb|CAA98621.1| USO1 [Saccharomyces cerevisiae] Length = 1790

3810.1 Best-BlastP=>>nrprot 53% Identities = 78/237 (32%), Positives = 123/237 (51%), Gaps = 22/237 (9%) ref|NP_721557.1| conserved hypothetical protein [Streptococcus mutans UA159] gb|AAN58863.1|AE014954_2 conserved hypothetical protein [Streptococcus mutans UA159] Length = 246

3811.1 Best-BlastP=>>nrprot 48% Identities = 43/154 (27%), Positives = 73/154 (47%), Gaps = 35/154 (22%) ref|ZP_00074907.1| COG0534: Na+-driven multidrug efflux pump [Trichodesmium erythraeum IMS101] Length = 931

3814.1 Best-BlastP=>>nrprot 98% Identities = 278/282 (98%), Positives = 280/282 (99%) gb|AAM73852.1|AF454863_1 putative lipase LipA [Legionella pneumophila] Length = 282

3815.2 Best-BlastP=>>nrprot 65% Identities = 41/81 (50%), Positives = 62/81 (76%), Gaps = 2/81 (2%) ref|NP_901660.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ59662.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 104

3816.2 Best-BlastP=>>nrprot 69% Identities = 121/232 (52%), Positives = 170/232 (73%) ref|NP_719120.1| CDP-diacylglycerol--serine O-phosphatidyltransferase, putative [Shewanella oneidensis MR-1] gb|AAN56634.1|AE015794_2 CDP-diacylglycerol--serine O-phosphatidyltransferase, putative [Shewanella oneidensis MR-1] Length = 269

3818.1 Best-BlastP=>>nrprot 81% Identities = 50/89 (56%), Positives = 73/89 (82%) ref|NP_900485.1| sugar transport PTS system phosphocarrier protein HPR [Chromobacterium violaceum ATCC 12472] gblAAQ58490.1| sugar transport PTS system phosphocarrier protein HPR [Chromobacterium violaceum ATCC 12472] Length = 89

3819.2 Best-BlastP=>>nrprot 76% Identities = 61/95 (64%), Positives = 76/95 (80%) dbj|BAC93211.1| putative sigma-54 modulation protein [Vibrio vulnificus YJ016] Length = 95

3821.1 Best-BlastP=>>nrprot No Hits found

3822.2 Best-BlastP=>>nrprot 41% Identities = 44/157 (28%), Positives = 74/157 (47%), Gaps = 16/157 (10%) ref|NP_863847.1| hypothetical protein [Pirellula sp.] emb|CAD71520.1| hypothetical protein [Pirellula sp.] Length = 171

3824.2 Best-BlastP=>>nrprot 56% Identities = 166/428 (38%), Positives = 244/428 (57%), Gaps = 12/428 (2%) ref|NP_820492.1| mesJ protein [Coxiella burnetii] RSA 493] gbl|AAO91006.1| mesJ protein [Coxiella burnetii] RSA 493] Length = 449

3826.1 Best-BlastP=>>nrprot 57% Identities = 129/323 (39%), Positives = 190/323 (58%), Gaps = 9/323 (2%) ref|NP_820009.1| birA bifunctional protein [Coxiella burnetii] RSA 493] gbl|AAO90523.1| birA bifunctional protein [Coxiella burnetii] RSA 493] Length = 323

3827.2 Best-BlastP=>>nrprot 49% Identities = 224/663 (33%), Positives = 330/663 (49%), Gaps = 66/663 (9%) ref|NP_106287.1| O-antigen acetylase [Mesorhizobium loti] dbj|BAB52073.1| O-antigen acetylase [Mesorhizobium loti] Length = 628

3830.2 Best-BlastP=>>nrprot No Hits found

3832.1 Best-BlastP=>>nrprot 41% Identities = 107/294 (36%), Positives = 168/294 (57%), Gaps = 16/294 (5%) ref|NP_899726.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] gbl|AAQ57736.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] Length = 415

3834.1 Best-BlastP=>>nrprot No Hits found

3835.2 Best-BlastP=>>nrprot 47% Identities = 66/245 (26%), Positives = 118/245 (48%), Gaps = 10/245 (4%) emb|CAA60105.1| artJ [Escherichia coli] Length = 243

3837.3 Best-BlastP=>>nrprot 12% Identities = 45/120 (37%), Positives = 61/120 (50%), Gaps = 8/120 (6%) gbl|AAH52346.1| 4921520G13Rik protein [Mus musculus] Length = 379

3838.3 Best-BlastP=>>nrprot 99% Identities = 710/718 (98%), Positives = 716/718 (99%) emb|CAD90951.1| LssB protein [Legionella pneumophila] Length = 718

384.3 Best-BlastP=>>nrprot 30% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gbl|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180

3840.1 Best-BlastP=>>nrprot 99% Identities = 352/355 (99%), Positives = 355/355 (100%) emb|CAD90958.1| LssD protein [Legionella pneumophila] Length = 378

3841.2 Best-BlastP=>>nrprot 91% Identities = 719/842 (85%), Positives = 774/842 (91%) emb|CAD90957.1| LssE protein [Legionella pneumophila] Length = 842

3846.2 Best-BlastP=>>nrprot 41% Identities = 205/677 (30%), Positives = 350/677 (51%), Gaps = 31/677 (4%) gbl|AAM82673.1| PacS [Synechococcus sp. PCC 7942] Length = 747

3849.1 Best-BlastP=>>nrprot 69% Identities = 117/228 (51%), Positives = 169/228 (74%), Gaps = 2/228 (0%) ref|ZP_00067594.1| COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Microbacter degradans 2-40] Length = 244

3850.1 Best-BlastP=>>nrprot 72% Identities = 82/139 (58%), Positives = 102/139 (73%) ref|ZP_00086776.1| COG1981: Predicted membrane protein [Pseudomonas fluorescens PfO-1] Length = 142

3851.1 Best-BlastP=>>nrprot 83% Identities = 43/56 (76%), Positives = 49/56 (87%) ref|NP_841467.1| Rubredoxin:Rubredoxin-type Fe(Cys)4 protein europaea ATCC 19718] emb|CAD853337.1| Rubredoxin:Rubredoxin-type Fe(Cys)4 protein [Nitrosomonas europaea ATCC 19718] Length = 62

3853.2 Best-BlastP=>>nrprot 74% Identities = 264/426 (61%), Positives = 318/426 (74%) ref|ZP_00133736.1| COG0001: Glutamate-1-semialdehyde aminotransferase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 426

3855.1 Best-BlastP=>>nrprot 59% Identities = 115/256 (44%), Positives = 157/256 (61%), Gaps = 1/256 (0%) ref|NP_251460.1| hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9I073|YR70_PSEAE Hypothetical protein PA2770 pir|A83301 hypothetical protein PA2770 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06158.1|AE004704_12 hypothetical protein PA2770 [Pseudomonas aeruginosa PAO1] Length = 259

3857.3 Best-BlastP=>>nrprot 99% Identities = 367/372 (98%), Positives = 371/372 (99%) gb|AAD42885.1|AF157018_1_PrpC [Legionella pneumophila] Length = 372

3859.2 Best-BlastP=>>nrprot 84% Identities = 308/442 (69%), Positives = 374/442 (84%), Gaps = 5/442 (1%) ref|NP_756738.1| ATP-dependent hsl protease ATP-binding subunit hslU [Escherichia coli CFT073] sp|Q8FB0|HSLU_ECOL6 ATP-dependent hsl protease ATP-binding subunit hslU [Escherichia coli CFT073] Length = 443

3860.2 Best-BlastP=>>nrprot 89% Identities = 146/180 (81%), Positives = 164/180 (91%) ref|NP_820986.1| protease HslVU, subunit HslV [Coxiella burnetii RSA 493] gb|AA091500.1| protease HslVU, subunit HslV [Coxiella burnetii RSA 493] Length = 181

3863.2 Best-BlastP=>>nrprot 99% Identities = 196/199 (98%), Positives = 198/199 (99%) sp|O32481|GRPE_LEGPN GRPE PROTEIN (HSP-70 COFACTOR) dbj|BAA22782.1| GrpE [Legionella pneumophila] Length = 199

3867.2 Best-BlastP=>>nrprot 72% Identities = 242/435 (55%), Positives = 325/435 (74%), Gaps = 1/435 (0%) gb|AK14074.1|AF303107_1 family II 2-keto-3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Xanthomonas campestris] Length = 478

3871.1 Best-BlastP=>>nrprot No Hits found

3872.1 Best-BlastP=>>nrprot No Hits found

3874.1 Best-BlastP=>>nrprot No Hits found

3876.1 Best-BlastP=>>nrprot 42% Identities = 49/160 (30%), Positives = 71/160 (44%), Gaps = 29/160 (18%) ref|ZP_00079746.1| COG3034: Uncharacterized protein conserved in bacteria [Geobacter metallireducens] Length = 175

3878.1 Best-BlastP=>>nrprot 23% Identities = 112/536 (20%), Positives = 244/536 (45%), Gaps = 42/536 (7%) gb|AO52540.1| similar to Entamoeba histolytica. Myosin heavy chain [Dictyostelium discoideum] Length = 915

3884.2 Best-BlastP=>>nrprot No Hits found

3887.1 Best-BlastP=>>nrprot 37% Identities = 87/397 (21%), Positives = 155/397 (39%), Gaps = 28/397 (7%) ref|NP_764987.1| multidrug resistance protein-like protein [Staphylococcus epidermidis ATCC 12228] gb|AA005031.1|AE016748_265 multidrug resistance protein-like protein [Staphylococcus epidermidis ATCC 12228] Length = 404

3888.1 Best-BlastP=>>nrprot No Hits found

3889.1 Best-BlastP=>>nprot 48% Identities = 75/257 (29%), Positives = 126/257 (49%), Gaps = 23/257 (8%) ref|NP_922978.1| hypothetical protein gll0032 [Gloeo**bacter** violaceus] dbj|BAC87973.1| gll|0032 [Gloeo**bacter** violaceus] Length = 267

389.3 Best-BlastP=>>nprot 61% Identities = 283/637 (44%), Positives = 401/637 (62%), Gaps = 10/637 (1%) ref|NP_840954.1| probable ATP-dependent DNA helicase-related protein [Nitrosomonas europaea ATCC 19718] emb|CAD84791.1| probable ATP-dependent DNA helicase-related protein [Nitrosomonas europaea ATCC 19718] Length = 646

3890.2 Best-BlastP=>>nprot No Hits found

3891.2 Best-BlastP=>>nprot 56% Identities = 85/194 (43%), Positives = 120/194 (61%), Gaps = 7/194 (3%) ref|NP_6998073.1| conserved hypothetical protein [Brucella suis 1330] gb|AAN29988.1| AE014408_2 conserved hypothetical protein [Brucella suis 1330] Length = 203

3892.3 Best-BlastP=>>nprot 55% Identities = 149/349 (42%), Positives = 207/349 (59%), Gaps = 3/349 (0%) ref|ZP_00008996.1| COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Rhodopseudomonas palustris] Length = 379

3895.2 Best-BlastP=>>nprot 48% Identities = 92/324 (28%), Positives = 160/324 (49%), Gaps = 11/324 (3%) ref|NP_819818.1| multidrug resistance protein [Coxiella burnetii RSA 493] gb|AAO90332.1| multidrug resistance protein [Coxiella burnetii RSA 493] Length = 331

3898.2 Best-BlastP=>>nprot No Hits found

3899.2 Best-BlastP=>>nprot No Hits found

39.1 Best-BlastP=>>nprot 96% Identities = 340/363 (93%), Positives = 352/363 (96%) emb|CAB60060.1| lvhB10 [Legionella pneumophila] Length = 363

390.2 Best-BlastP=>>nprot 86% Identities = 80/106 (75%), Positives = 97/106 (91%) sp|P08811|FER_PEST Ferredoxin [3Fe-4S][4Fe-4S] - Pseudomonas stutzeri prf|1410240A ferredoxin Length = 106

3901.2 Best-BlastP=>>nprot 75% Identities = 152/272 (55%), Positives = 204/272 (75%) ref|NP_250460.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9I2X0|YH69_PSEAE Hypothetical UPF0085 protein PA1769 pir|D83425 conserved hypothetical protein PA1769 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05158.1|AE004602_9 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 274

3902.3 Best-BlastP=>>nprot 79% Identities = 312/481 (64%), Positives = 382/481 (79%) ref|ZP_00081898.1| COG2079: Uncharacterized protein involved in propionate catabolism [Geobacter metallireducens] Length = 481

3904.3 Best-BlastP=>>nprot 54% Identities = 222/592 (37%), Positives = 332/592 (56%), Gaps = 16/592 (2%) ref|NP_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish7) gb|AA02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589

3908.3 Best-BlastP=>>nprot No Hits found

3909.3 Best-BlastP=>>nprot No Hits found

3911.2 Best-BlastP=>>nprot 78% Identities = 384/621 (61%), Positives = 489/621 (78%), Gaps = 3/621 (0%) sp|P58480|HTPG_SALTY Chaperone protein htpG (Heat shock protein htpG) (High temperature protein G) Length = 624

3913.2 Best-BlastP=>>nprot 71% Identities = 194/356 (54%), Positives = 267/356 (75%) ref|NP_819581.1| rod shape-determining protein RodA [Coxiella burnetii RSA 493] gb|AAO90095.1| rod shape-determining protein RodA [Coxiella burnetii RSA 493] Length = 359

3914.3 Best-BlastP=>>nrprot 65% Identities = 286/604 (47%), Positives = 407/604 (67%), Gaps = 2/604 (0%) ref|NP_819582.1| penicillin-binding protein 2 [Coxiella burnetii RSA 493] gb|AAO90096.1| penicillin-binding protein 2 [Coxiella burnetii RSA 493] Length = 612

3916.3 Best-BlastP=>>nrprot 72% Identities = 267/417 (64%), Positives = 331/417 (79%) ref|NP_253428.1| polyribonucleotide nucleotidyltransferase [Pseudomonas aeruginosa PA01] pirl|C83052 polyribonucleotide nucleotidyltransferase PA4740 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08126.1|AE0048888_1 polyribonucleotide nucleotidyltransferase [Pseudomonas aeruginosa PAO1] Length = 701

3917.1 Best-BlastP=>>nrprot 70% Identities = 56/88 (63%), Positives = 65/88 (73%) ref|ZP_00091229.1| COG0184: Ribosomal protein S15P/S13E [Azotobacter vinelandii] Length = 132

3919.1 Best-BlastP=>>nrprot 61% Identities = 138/299 (46%), Positives = 188/299 (62%), Gaps = 11/299 (3%) ref|XP_306459.1| ENSANGP00000001690 [Anopheles gambiae] gb|EAA02278.1| ENSANGP00000001690 [Anopheles gambiae str. PEST] Length = 309

3920.1 Best-BlastP=>>nrprot 64% Identities = 60/113 (53%), Positives = 80/113 (70%), Gaps = 3/113 (2%) ref|NP_840836.1| Ribosome-binding factor A [Nitrosomonas europaea ATCC 19718] sp|Q882WC9|RBF4_NITEU Ribosome-binding factor A emb|CAD84673.1| Ribosome-binding factor A [Nitrosomonas europaea ATCC 19718] Length = 117

3923.2 Best-BlastP=>>nrprot 63% Identities = 244/604 (40%), Positives = 394/604 (65%), Gaps = 9/604 (1%) ref|NP_622330.1| predicted nucleoside-diphosphate sugar epimerases [Thermoanaerobacter tengcongensis] gb|AAW23934.1| predicted nucleoside-diphosphate sugar epimerases [Thermoanaerobacter tengcongensis] Length = 623

3924.2 Best-BlastP=>>nrprot 57% Identities = 90/279 (32%), Positives = 162/279 (58%), Gaps = 8/279 (2%) ref|NP_348443.1| Conserved membrane protein, possible 4-hydroxybenzoate octaprenyltransferase [Clostridium acetobutylicum] pir|D97124 conserved membrane protein, probable 4-hydroxybenzoate octaprenyltransferase CAC1818 [imported] - Clostridium acetobutylicum gb|AAK79783.1|AE007691_1 Conserved membrane protein, possible 4-hydroxybenzoate octaprenyltransferase [Clostridium acetobutylicum] Length = 290

3925.2 Best-BlastP=>>nrprot No Hits found

3927.2 Best-BlastP=>>nrprot 67% Identities = 228/453 (50%), Positives = 305/453 (67%), Gaps = 34/453 (7%) ref|NP_820835.1| peptide ABC transporter, permease protein, putative [Coxiella burnetii RSA 493] gb|AAO91349.1| peptide ABC transporter, permease protein, putative [Coxiella burnetii RSA 493] Length = 465

3928.1 Best-BlastP=>>nrprot 99% Identities = 593/596 (99%) emb|CAA67994.1| oxaloacetate decarboxylase alpha-chain [Legionella pneumophila] Length = 596

3929.2 Best-BlastP=>>nrprot 99% Identities = 542/543 (99%), Positives = 542/543 (99%) sp|P21347|PROA_LEGPN Zinc metalloproteinase precursor (PEP1) (PRO A) pirl|A35265 zinc metalloproteinase (EC 3.4.24.-) precursor - Legionella pneumophila gb|AAA25301.1| zinc metalloprotease precursor (EC 3.4.24.) Length = 543

393.1 Best-BlastP=>>nrprot 67% Identities = 67/107 (62%), Positives = 87/107 (81%) ref|NP_747247.1| (d) nucleoside polyphosphate hydrolase, putative [Pseudomonas putida KT2440] sp|Q88CN4|NUDH_PSEPK Probable (d) nucleoside polyphosphate hydrolase gb|AN70711.1|AE016714_9 (d) nucleoside polyphosphate hydrolase, putative [Pseudomonas putida KT2440] Length = 159

3933.3 Best-BlastP=>>nrprot No Hits found

3936.2 Best-BlastP=>>nrprot 31% Identities = 95/227 (41%), Positives = 131/227 (57%), Gaps = 29/227 (12%) sp|Q9ZB07|PURQ_LACLC Phosphoribosylformylglycaminide synthase I (FGAM synthase I) pir|T51700 phosphoribosylformylglycaminide synthase (EC 6.3.5.3) component I [similarity] - *Lactococcus lactis* gb|AAD12625.1| phosphoribosylformylglycaminide synthetase I [*Lactococcus lactis*] Length = 226

3937.2 Best-BlastP=>>nrprot 65% Identities = 216/436 (49%), Positives = 286/436 (65%), Gaps = 4/436 (0%) ref|ZP_00077753.1| COG0151: Phosphoribosylamine-glycine ligase [Methanoscarcina barkeri] Length = 433

3938.2 Best-BlastP=>>nrprot 65% Identities = 75/186 (40%), Positives = 127/186 (68%), Gaps = 4/186 (2%) ref|NP_632467.1| Phosphoribosylglycaminide formyltransferase [Methanoscarcina mazei] Goe1 gb|AAM30139.1| Phosphoribosylglycaminide formyltransferase [Methanoscarcina mazei] Goe1 Length = 202

3942.2 Best-BlastP=>>nrprot 76% Identities = 186/311 (59%), Positives = 241/311 (77%), Gaps = 2/311 (0%) ref|ZP_00065258.1| COG2025: Electron transfer flavoprotein, alpha subunit [Microbulbifer degradans 2-40] Length = 312

3950.2 Best-BlastP=>>nrprot 46% Identities = 148/462 (32%), Positives = 248/462 (53%), Gaps = 23/462 (4%) ref|NP_488265.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AB2334 hypothetical protein ali4225 [imported] - *Nostoc* sp. (strain PCC 7120) dbj|BAB75924.1| ORF_ID:ali4225 hypothetical protein [Nostoc sp. PCC 7120] Length = 565

3953.1 Best-BlastP=>>nrprot 74% Identities = 231/395 (58%), Positives = 292/395 (73%), Gaps = 7/395 (1%) ref|NP_840860.1| Aminotransferases class-I [Nitrosomonas europaea ATCC 19718] emb|CAD84697.1| Aminotransferases class-I [*Nitrosomonas europaea* ATCC 19718] Length = 397

3956.2 Best-BlastP=>>nrprot 50% Identities = 71/224 (31%), Positives = 124/224 (55%), Gaps = 11/224 (4%) ref|NP_841085.1| SURF1 family [Nitrosomonas europaea ATCC 19718] emb|CAD84923.1| SURF1 family [*Nitrosomonas europaea* ATCC 19718] Length = 239

3957.1 Best-BlastP=>>nrprot 67% Identities = 28/65 (43%), Positives = 46/65 (70%) ref|NP_518489.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD13896.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 69

3958.1 Best-BlastP=>>nrprot 42% Identities = 76/80 (95%), Positives = 77/80 (96%) gb|AAO61477.1| unknown [Legionella pneumophila] Length = 80

3959.2 Best-BlastP=>>nrprot 18% Identities = 60/197 (30%), Positives = 98/197 (49%), Gaps = 18/197 (9%) ref|NP_660278.2| similar to RIKEN cDNA 1700007B22 [Homo sapiens] gb|AAH24189.2| Similar to RIKEN cDNA 1700007B22 [Homo sapiens] Length = 345

396.4 Best-BlastP=>>nrprot 68% Identities = 152/296 (51%), Positives = 203/296 (68%), Gaps = 2/296 (0%) ref|NP_798532.1| L-asparaginase I [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60416.1| L-asparaginase I [Vibrio parahaemolyticus] Length = 337

3960.2 Best-BlastP=>>nrprot 57% Identities = 37/110 (33%), Positives = 65/110 (59%), Gaps = 1/110 (0%) ref|NP_819167.1| cell division protein FtsL [Coxiella burnetii RSA 493] gb|AAO89681.1| cell division protein FtsL [Coxiella burnetii RSA 493] Length = 115

3964.1 Best-BlastP=>>nrprot 72% Identities = 166/311 (53%), Positives = 224/311 (72%), Gaps = 7/311 (2%) ref|NP_930870.1| S-adenosyl-methyltransferase Mraw [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16035.1| S-adenosyl-methyltransferase Mraw [Photorhabdus luminescens subsp. laumondii TTO1] Length = 314

3965.1 Best-BlastP=> >nrprot 73% Identities = 89/152 (58%), Positives = 113/152 (74%) ref|NP_819165.1| conserved hypothetical protein TIGR00242 [Coxiella burnetii RSA 493] gb|AAO89679.1| conserved hypothetical protein TIGR00242 [Coxiella burnetii RSA 493] Length = 152

3966.1 Best-BlastP=> >nrprot 64% Identities = 116/251 (46%), Positives = 166/251 (66%), Gaps = 4/251 (1%) ref|ZP_00060306.1| COG1521. Putative transcriptional regulator, homolog of Bvg accessory factor [Clostridium thermocellum ATCC 27405] Length = 255

3967.1 Best-BlastP=> >nrprot 48% Identities = 73/139 (52%), Positives = 91/139 (65%), Gaps = 1/139 (0%) ref|NP_819361.1| conserved domain protein [Coxiella burnetii RSA 493] gb|AAO89875.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 214

3968.1 Best-BlastP=> >nrprot 39% Identities = 35/77 (45%), Positives = 48/77 (62%), Gaps = 3/77 (3%) ref|NP_760035.1| Cytochrome c5 [Vibrio vulnificus CMCP6] gb|AAO09562.1|AE016800_167 Cytochrome c5 [Vibrio vulnificus CMCP6] dbj|BAC92805.1| cytochrome c5 [Vibrio vulnificus YJ016] Length = 150

3969.1 Best-BlastP=> >nrprot 49% Identities = 69/204 (33%), Positives = 115/204 (56%), Gaps = 5/204 (2%) ref|NP_252040.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|C83227 hypothetical protein PA3350 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG06738.1|AE004757_7 hypothetical protein PA3350 [Pseudomonas aeruginosa PAO1] Length = 232

397.2 Best-BlastP=> >nrprot 59% Identities = 68/133 (51%), Positives = 100/133 (75%) ref|ZP_00043701.1| COG1974: SOS-response transcriptional repressors (ReCA-mediated autopptidases) [Magnetococcus sp. MC-1] Length = 238

3970.1 Best-BlastP=> >nrprot 37% Identities = 23/57 (40%), Positives = 40/57 (70%) ref|ZP_00084200.1| COG2747: Negative regulator of flagellin synthesis (anti-sigma28 factor) [Pseudomonas fluorescens FfO-1] Length = 131

3971.2 Best-BlastP=> >nrprot 43% Identities = 41/149 (27%), Positives = 72/149 (48%), Gaps = 6/149 (4%) ref|ZP_00136724.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 156

3972.2 Best-BlastP=> >nrprot 71% Identities = 139/251 (55%), Positives = 178/251 (70%), Gaps = 5/251 (1%) ref|NP_819867.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Coxiella burnetii RSA 493] gb|AAO90381.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Coxiella burnetii RSA 493] Length = 254

3974.2 Best-BlastP=> >nrprot 64% Identities = 76/181 (41%), Positives = 118/181 (65%), Gaps = 1/181 (0%) ref|NP_252535.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|A83164 hypothetical protein PA3846 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG07233.1|AE004802_2 hypothetical protein PA3846 [Pseudomonas aeruginosa PAO1] Length = 180

3977.2 Best-BlastP=> >nrprot 23% Identities = 105/397 (26%), Positives = 174/397 (43%), Gaps = 43/397 (10%) ref|ZP_00008208.1| COG0665: Glycine/D-amino acid oxidases (deaminating) [Rhodobacter sphaeroides] Length = 533

3979.2 Best-BlastP=> >nrprot 61% Identities = 270/546 (49%), Positives = 356/546 (65%), Gaps = 14/546 (2%) ref|NP_298274.1| gamma-glutamyltranspeptidase [Xylella fastidiosa 9a5c] pir|G82738 gamma-glutamyltranspeptidase XF0984 [Imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83794.1|AE003936_8 gamma-glutamyltranspeptidase [Xylella fastidiosa 9a5c] Length = 603

398.2 Best-BlastP=> >nrprot 62% Identities = 203/420 (48%), Positives = 267/420 (63%), Gaps = 7/420 (1%) ref|ZP_00043700.1| COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Magnetococcus sp. MC-1] Length = 421

3980.1 Best-BlastP=> >nrprot 68% Identities = 90/158 (56%), Positives = 116/158 (73%) ref|ZP_00021201.1| COG0669: Phosphopantetheine adenyltransferase [Ralstonia metallidurans] Length = 161

3982.2 Best-BlastP=>>nrprot 55% Identities = 62/185 (33%), Positives = 110/185 (59%), Gaps = 4/185 (2%) ref|NP_820808.1| outer membrane lipoprotein LolB, putative [Coxiella burnetii RSA 493] gb|AAO91322.1| outer membrane lipoprotein LolB, putative [Coxiella burnetii RSA 493] Length = 210

3985.1 Best-BlastP=>>nrprot 34% Identities = 40/148 (27%), Positives = 70/148 (47%) gb|AAC01725.1| rifamycin efflux protein [Amycolatopsis mediterranei] Length = 522

3986.1 Best-BlastP=>>nrprot 59% Identities = 155/374 (41%), Positives = 222/374 (59%), Gaps = 11/374 (2%) ref|NP_485927.1| hypothetical protein [Nostoc sp. PCC 7120] pir|A|2041 hypothetical protein all1887 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB73586.1| ORF_ID:all1887~hypothetical protein [Nostoc sp. PCC 7120] Length = 375

3988.3 Best-BlastP=>>nrprot 21% Identities = 60/228 (26%), Positives = 106/228 (46%), Gaps = 16/228 (7%) dbj|BAB84935.1| FLJ00180 protein [Homo sapiens] Length = 499

3989.1 Best-BlastP=>>nrprot 70% Identities = 84/147 (57%), Positives = 106/147 (72%), Gaps = 3/147 (2%) ref|NP_457097.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_461503.1| putative Cytosine/adenosine deaminase [Salmonella typhimurium LT2] ref|NP_804165.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi [Ty2] pir|AF0827 conserved hypothetical protein STY2814 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAU21462.1| putative cytosine/adenosine deaminase [Salmonella typhimurium LT2] emb|CAD02770.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO68014.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 183

399.2 Best-BlastP=>>nrprot 20% Identities = 79/403 (19%), Positives = 171/403 (42%), Gaps = 54/403 (13%) gb|EAA16038.1| repeat organellar protein-related [Plasmidium yoelii yoelii] Length = 1441

3991.3 Best-BlastP=>>nrprot 10% Identities = 35/108 (32%), Positives = 60/108 (55%), Gaps = 4/108 (3%) ref|XP_316738.1| ENSANGP00000016119 [Anopheles gambiae] gb|EAA11974.1| ENSANGP00000016119 [Anopheles gambiae str. PEST] Length = 602

3993.2 Best-BlastP=>>nrprot No Hits found

3994.5 Best-BlastP=>>nrprot 29% Identities = 41/133 (30%), Positives = 65/133 (48%), Gaps = 27/133 (20%) dbj|BAB21508.1| protein-glutaminase [Chryseobacterium proteolyticum] Length = 320

3995.5 Best-BlastP=>>nrprot 29% Identities = 85/264 (32%), Positives = 125/264 (47%), Gaps = 26/264 (9%) ref|NP_810963.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO77157.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Length = 425

3996.2 Best-BlastP=>>nrprot No Hits found

3998.3 Best-BlastP=>>nrprot 42% Identities = 36/142 (25%), Positives = 66/142 (46%), Gaps = 10/142 (7%) ref|NP_751974.1| Putative glutamate dehydrogenase [Escherichia coli CFT073] gb|AAN78518.1|AE016755_18 Putative glutamate dehydrogenase [Escherichia coli CFT073] Length = 678

3999.3 Best-BlastP=>>nrprot 99% Identities = 641/644 (99%), Positives = 642/644 (99%) sp|O32482|DNAK_LGPN Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) dbj|BAA22783.1| DnaK [Legionella pneumophila] Length = 644

4.1 Best-BlastP=> >nrprot 59% Identities = 120/298 (40%), Positives = 181/298 (60%), Gaps = 1/298 (0%) ref|NP_907748.1| conserved hypothetical protein [Wolinella succinogenes] emb|CAE10648.1| conserved hypothetical protein [Wolinella succinogenes] Length = 332

400.1 Best-BlastP=> >nrprot 30% Identities = 45/177 (25%), Positives = 80/177 (45%), Gaps = 25/177 (14%) ref|NP_587991.1| hypothetical structural protein [Schizosaccharomyces pombe] pir|T41077 hypothetical structural protein - fission yeast (Schizosaccharomyces pombe) emb|CAB53076.1| SPCC16A11.04 [Schizosaccharomyces pombe] Length = 1010

4000.2 Best-BlastP=> >nrprot 45% Identities = 42/110 (38%), Positives = 64/110 (58%), Gaps = 5/110 (4%) ref|NP_925923.1| MarR family transcriptional regulatory protein [Gloeo bacter violaceus] dbj|BAC90918.1| MarR family transcriptional regulatory protein [Gloeo bacter violaceus] Length = 143

4002.2 Best-BlastP=> >nrprot 24% Identities = 99/340 (29%), Positives = 154/340 (45%), Gaps = 53/340 (15%) ref|NP_623349.1| Cell division protein Ftsl/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] gb|AAM24853.1| Cell division protein Ftsl/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] Length = 678

4003.1 Best-BlastP=> >nrprot 50% Identities = 151/498 (30%), Positives = 248/498 (49%), Gaps = 51/498 (10%) ref|ZP_00112433.1| COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Nostoc punctiforme] Length = 544

4004.2 Best-BlastP=> >nrprot 61% Identities = 244/575 (42%), Positives = 366/575 (63%), Gaps = 8/575 (1%) ref|NP_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589

4005.2 Best-BlastP=> >nrprot 76% Identities = 309/502 (61%), Positives = 381/502 (75%), Gaps = 7/502 (1%) gb|AAP40013.1| lysine tRNA synthetase [Citrobacter freundii] Length = 505

4009.1 Best-BlastP=> >nrprot 85% Identities = 254/332 (76%), Positives = 288/332 (86%) ref|NP_457439.1| peptide chain release factor 2 (RF-2) [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_806651.1| peptide chain release factor 2 [Salmonella enterica subsp. enterica serovar Typhi Ty2] sp|P28353|RF2_SALTY Peptide chain release factor 2 (RF-2) pir|A36480 translation releasing factor RF-2 - Salmonella typhimurium pir|AG0871 peptide chain release factor 2 (RF-2) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AA72914.1| peptide chain release factor 2 emb|CAD02871.1| peptide chain release factor 2 (RF-2) [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO70511.1| peptide chain release factor 2 [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 365

401.2 Best-BlastP=> >nrprot 44% Identities = 128/335 (38%), Positives = 180/335 (53%), Gaps = 12/335 (3%) ref|ZP_00005503.1| hypothetical protein [Rhodobacter sphaeroides] Length = 458

4010.1 Best-BlastP=> >nrprot 42% Identities = 26/118 (22%), Positives = 58/118 (49%), Gaps = 13/118 (11%) ref|NP_903543.1| hypothetical protein CV3873 [Chromobacterium violaceum ATCC 12472] gb|AAQ61535.1| hypothetical protein CV3873 [Chromobacterium violaceum ATCC 12472] Length = 117

4012.1 Best-BlastP=>>nrprot 54% Identities = 98/248 (39%), Positives = 150/248 (60%), Gaps = 14/248 (5%) ref|NP_250152.1| probable chemotaxis protein [Pseudomonas aeruginosa PA01] ref|ZP_00139088.1| COG1360: Flagellar motor protein [Pseudomonas aeruginosa UCBPP-PA14] pir|T46617 probable chemotaxis protein PA1461 [imported] - Pseudomonas [Pseudomonas aeruginosa] gb|AAG04850.1|AE004575_9 probable chemotaxis protein [Pseudomonas aeruginosa PAO1] Length = 296

4013.1 Best-BlastP=>>nrprot 67% Identities = 129/244 (52%), Positives = 175/244 (71%) ref|NP_746451.1| flagellar motor protein MotA [Pseudomonas putida KT2440] gb|AAN69915.1|AE016630_6 flagellar motor protein MotA [Pseudomonas putida KT2440] Length = 246

4014.1 Best-BlastP=>>nrprot 97% Identities = 231/238 (97%), Positives = 234/238 (98%) emb|CAA67397.1| sigma factor 28 [Legionella pneumophila] Length = 238

4015.1 Best-BlastP=>>nrprot 76% Identities = 119/229 (51%), Positives = 178/229 (77%) gb|AAC62540.2| MotR [Pseudomonas aeruginosa] Length = 275

4016.1 Best-BlastP=>>nrprot 49% Identities = 124/284 (43%), Positives = 187/284 (65%), Gaps = 5/284 (1%) gb|AAF32412.1| flagellar biosynthesis protein FlhF [Vibrio parahaemolyticus] Length = 503

4017.4 Best-BlastP=>>nrprot 80% Identities = 433/701 (61%), Positives = 560/701 (79%), Gaps = 9/701 (1%) ref|NP_250143.1| flagellar biosynthesis protein FlhA [Pseudomonas aeruginosa PA01] ref|ZP_00139079.1| COG1298: Flagellar biosynthesis pathway, component FlhA [Pseudomonas aeruginosa UCBPP-PA14] pir|F83465 flagellar biosynthesis protein FlhA PA1452 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04841.1|AE004574_12 flagellar biosynthesis protein FlhA [Pseudomonas aeruginosa PAO1] Length = 707

402.2 Best-BlastP=>>nrprot No Hits found

4020.2

4021.2 Best-BlastP=>>nrprot 48% Identities = 177/535 (33%), Positives = 277/535 (51%), Gaps = 29/535 (5%) ref|NP_819244.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89758.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 578

4023.2 Best-BlastP=>>nrprot 41% Identities = 53/162 (32%), Positives = 81/162 (50%), Gaps = 3/162 (1%) ref|NP_643713.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] sp|Q8PH54|YY06_XANAC Hypothetical UPF0149 protein XAC3406 gb|AAV38249.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 180

4025.1 Best-BlastP=>>nrprot 56% Identities = 161/389 (41%), Positives = 227/389 (58%), Gaps = 12/389 (3%) ref|NP_253910.1| ubiH protein [Pseudomonas aeruginosa PA01] pir|G82992 ubiH protein PA5223 [imported] - Pseudomonas aeruginosa (strain PAO1) Length = 394

4026.2 Best-BlastP=>>nrprot 59% Identities = 171/394 (43%), Positives = 229/394 (58%), Gaps = 9/394 (2%) ref|NP_716409.1| oxidoreductase, FAD-binding, UbiH/Coq6 family [Shewanella oneidensis MR-1] gb|AAN53854.1|AE015522_9 oxidoreductase, FAD-binding, UbiH/Coq6 family [Shewanella oneidensis MR-1] Length = 407

4030.1 Best-BlastP=>>nrprot 35% Identities = 33/123 (26%), Positives = 54/123 (43%), Gaps = 30/123 (24%) ref|NP_604443.1| dystonin isoform b; bullous pemphigoid antigen 1; dystonia musculorum [Mus musculus] sp|Q91ZU6|BPA1_MOUSE Bullous pemphigoid antigen 1, isoforms 1/2/3/4 (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonin) gb|AAK83384.1|AF396879_1 bullous pemphigoid antigen 1-b [Mus musculus] Length = 7389

4032.3 Best-BlastP=>>nrprot 76% Identities = 179/322 (55%), Positives = 242/322 (75%), Gaps = 7/322 (2%) ref|ZP_00090005.1| hypothetical protein [Azotobacter vinelandii] Length = 328

4035.1 Best-BlastP=>>nrprot 55% Identities = 47/121 (38%), Positives = 68/121 (56%), Gaps = 7/121 (5%) gb|AAL25256.1| Trak [Legionella pneumophila] Length = 114

4036.2 Best-BlastP=>>nrprot 50% Identities = 30/99 (30%), Positives = 48/99 (48%), Gaps = 6/99 (6%) ref|NP_903527.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61519.2| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 576

4037.2 Best-BlastP=>>nrprot 75% Identities = 42/78 (53%), Positives = 60/78 (76%) ref|NP_759375.1| Predicted transcriptional regulator [Vibrio vulnificus CMCP6] gb|AAO008902.1|AE016798_62 Predicted transcriptional regulator [Vibrio vulnificus CMCP6] Length = 85

4039.2 Best-BlastP=>>nrprot 62% Identities = 206/434 (47%), Positives = 273/434 (62%), Gaps = 5/434 (1%) ref|NP_932051.1| HipA protein [Photorhabdus luminescens subsp. laumontii TTO1]胚|CAE17272.1| HipA protein [Photorhabdus luminescens subsp. laumontii TTO1] Length = 439

4040.1 Best-BlastP=>>nrprot 32% Identities = 19/53 (35%), Positives = 32/53 (60%), Gaps = 2/53 (3%) ref|NP_297921.1| phage-related integrase [Xylella fastidiosa 9a5c] pir|E82782 phage-related integrase XF0631 [imported] - Xylella fastidiosa (strain 9a5c) gb|AF83441.1|AE003908_9 phage-related integrase [Xylella fastidiosa 9a5c] Length = 413

4041.1 Best-BlastP=>>nrprot No Hits found

4042.1 Best-BlastP=>>nrprot 84% Identities = 169/231 (73%), Positives = 198/231 (85%) ref|NP_435396.1| hypothetical protein [Sinorhizobium meliloti] pir|FG9280 hypothetical protein SMA0280 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA_gb|AAK64808.1| hypothetical protein [Sinorhizobium meliloti] Length = 262

4043.1 Best-BlastP=>>nrprot 65% Identities = 63/126 (50%), Positives = 88/126 (69%), Gaps = 5/126 (3%) ref|NP_435397.1| putative regulator, MerR family [Sinorhizobium meliloti] pir|G95280 probable regulator, MerR family [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA_gb|AAK64809.1| putative regulator, MerR family [Sinorhizobium meliloti] Length = 134

4045.2 Best-BlastP=>>nrprot No Hits found

4047.3 Best-BlastP=>>nrprot 57% Identities = 142/327 (43%), Positives = 195/327 (59%), Gaps = 7/327 (2%) ref|NP_819580.1| lytic murein transglycosylase [Coxiella burnetii RSA 493] gb|AO009094.1| lytic murein transglycosylase [Coxiella burnetii RSA 493] Length = 334

4048.3 Best-BlastP=>>nrprot 86% Identities = 443/598 (74%), Positives = 520/598 (86%) ref|ZP_00090179.1| COG0481: Membrane GTPase LepA [Azotobacter vinelandii] Length = 599

405.3 Best-BlastP=>>nrprot 11% Identities = 44/140 (31%), Positives = 73/140 (52%), Gaps = 4/140 (2%) pir|OXRTGU L-gulonolactone oxidase (EC 1.1.3.8) - rat dbj|BAA02232.1| L-gulono-gamma-lactone oxidase [Rattus norvegicus] Length = 440

4050.1 Best-BlastP=>>nrprot 73% Identities = 133/254 (52%), Positives = 184/254 (72%), Gaps = 9/254 (3%) ref|NP_820098.1| signal peptidase I [Coxiella burnetii RSA 493] gb|AAO90612.1| signal peptidase I [Coxiella burnetii RSA 493] Length = 259

4051.2 Best-BlastP=>>nrprot 51% Identities = 37/118 (31%), Positives = 67/118 (56%), Gaps = 6/118 (5%) ref|NP_842322.1| possible transmembrane protein [Nitrosomonas europaea ATCC 19718] Length = 126

4054.2 Best-BlastP=>>nrprot 68% Identities = 122/222 (54%), Positives = 155/222 (69%), Gaps = 4/222 (1%) ref|NP_716968.1| ribonuclease III [Shewanella oneidensis MR-1] Length = 226

4055.1 Best-BlastP=>>nrprot 67% Identities = 309/628 (49%), Positives = 418/628 (66%), Gaps = 14/628 (2%) ref|ZP_00092302.1| COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Azotobacter vinelandii] Length = 830

4056.2 Best-BlastP=>>nrprot 75% Identities = 247/407 (60%), Positives = 308/407 (75%) ref|NP_052356.1| unnamed protein product [Coxiella burnetii] pir|[S38238 hypothetical protein - Coxiella burnetii] emb|[CAA53126.1| unnamed protein product [Coxiella burnetii] emb|[CAA63678.1| orf410 [Coxiella burnetii] Length = 410

4058.2 Best-BlastP=>>nrprot No Hits found

406.1 Best-BlastP=>>nrprot 51% Identities = 95/241 (39%), Positives = 143/241 (59%), Gaps = 6/241 (2%) ref|NP_107761.1| unknown protein [Mesorhizobium loti] dbj|[BAB53547.1| unknown protein [Mesorhizobium loti] Length = 273

4060.1 Best-BlastP=>>nrprot 66% Identities = 208/400 (52%), Positives = 273/400 (68%), Gaps = 5/400 (1%) ref|NP_747386.1| phosphopantethenate-cysteine ligase [Pseudomonas putida KT2440] Length = 403

4061.1 Best-BlastP=>>nrprot 79% Identities = 108/147 (73%), Positives = 121/147 (82%) ref|ZP_00134300.1| COG0756: dUTPase [Actinobacillus pleuropneumoniae serovar 1 str.] Length = 151

4063.1 Best-BlastP=>>nrprot 66% Identities = 229/455 (50%), Positives = 310/455 (68%) ref|NP_747389.1| phosphomannomutase [Pseudomonas putida KT2440] sp|[Q88C93|ALGC_PSEPK Phosphomannomutase/phosphoglucomutase (PMM / PGM) gb|[AN70853.1|AE016729_11 phosphomannomutase [Pseudomonas putida KT2440] Length = 463

4065.3 Best-BlastP=>>nrprot 50% Identities = 181/557 (32%), Positives = 290/557 (52%), Gaps = 17/557 (3%) ref|NP_819579.1| TPR domain protein [Coxiella burnetii RSA 493] gb|[AO90093.1| TPR domain protein [Coxiella burnetii RSA 493] Length = 561

4066.2 Best-BlastP=>>nrprot 69% Identities = 102/190 (53%), Positives = 136/190 (71%), Gaps = 2/190 (1%) ref|NP_928489.1| hypothetical protein [Photobacterium luminescens subsp. laumontii] TTO1] emb|[CAE13471.1| unnamed protein product [Photobacterium luminescens subsp. laumontii] TTO1] Length = 197

4067.2 Best-BlastP=>>nrprot No Hits found

4068.2 Best-BlastP=>>nrprot 56% Identities = 174/381 (45%), Positives = 240/381 (62%), Gaps = 6/381 (1%) ref|NP_296878.1| sodium:dicarboxylate symporter family protein [Chlamydia muridarum] gb|[AAF73565.1| sodium:dicarboxylate symporter family protein [Chlamydia muridarum] Length = 415

407.4 Best-BlastP=>>nrprot 78% Identities = 295/449 (65%), Positives = 356/449 (79%) ref|NP_253299.1| DNA repair protein RadA [Pseudomonas aeruginosa PA01] sp|[P96963|RADAA_PSEAE DNA repair protein radA homolog (DNA repair protein sms homolog) pir|[A83069 DNA repair protein RadA PA4609 [imported] - Pseudomonas aeruginosa [Pseudomonas aeruginosa PAO1] Length = 453

4070.3

Best-BlastP=>>nrprot 82% Identities = 322/464 (69%), Positives = 387/464 (83%) ref|NP_415450.1| asparagine tRNA synthetase [Escherichia coli K12] ref|NP_752997.1| Asparaginyl-tRNA synthetase [Escherichia coli CFT073] ref|NP_836636.1| asparagine tRNA synthetase [Shigella flexneri 2a str. 2457T] sp|P17242|SYN_ECOLI Asparaginyl-tRNA synthetase (Asparagine-tRNA ligase) (AsnRS) pir|SYECNT asparagine-tRNA ligase (EC 6.1.1.22) - Escherichia coli (strain K-12) emb|CAA48274.1| Asparaginyl-tRNA synthetase [Escherichia coli] gb|AAA24666.1| asparaginyl-tRNA synthetase (asnS) dbj|BAA35682.1| Asparaginyl-tRNA synthetase (EC 6.1.1.22) (asparagine-tRNA ligase) (asnRS). [Escherichia coli K12] gb|AAC74016.1| asparagine tRNA synthetase [Escherichia coli K12] gb|AN79540.1|AE016758_144 Asparaginyl-tRNA synthetase [Escherichia coli CFT073] gb|AAP16442.1| asparagine tRNA synthetase [Shigella flexneri 2a str. 2457T] Length = 466

4071.1 Best-BlastP=>>nrprot No Hits found

4072.1 Best-BlastP=>>nrprot 98% Identities = 215/218 (98%), Positives = 216/218 (99%) gb|AAC32842.1| unknown [Legionella pneumophila] Length = 218

4073.1 Best-BlastP=>>nrprot 99% Identities = 355/357 (99%), Positives = 356/357 (99%) gb|AAC32841.1| unknown [Legionella pneumophila] Length = 357

4075.3 Best-BlastP=>>nrprot 58% Identities = 69/160 (43%), Positives = 93/160 (58%), Gaps = 4/160 (2%) ref|ZP_00051893.1| COGG3012: Uncharacterized protein conserved in bacteria [Magnetospirillum magnetotacticum] Length = 163

4076.1 Best-BlastP=>>nrprot No Hits found

4078.1 Best-BlastP=>>nrprot 70% Identities = 227/395 (57%), Positives = 303/395 (76%), Gaps = 1/395 (0%) ref|ZP_00031357.1| COGG0038: Chloride channel protein EriC [Burkholderia fungorum] Length = 443

408.3 Best-BlastP=>>nrprot 47% Identities = 152/478 (31%), Positives = 258/478 (53%), Gaps = 28/478 (5%) ref|NP_820790.1| outer membrane efflux family protein [Coxiella burnetii RSA 493] gb|AO91304.1| outer membrane efflux family protein [Coxiella burnetii RSA 493] Length = 507

4080.2 Best-BlastP=>>nrprot 89% Identities = 377/385 (97%), Positives = 381/385 (98%) gb|AAD47247.1| putative transport protein [Legionella pneumophila] Length = 387

4082.2 Best-BlastP=>>nrprot 34% Identities = 78/288 (27%), Positives = 138/288 (47%), Gaps = 2/288 (0%) ref|NP_931673.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE16879.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii TTO1] Length = 833

4083.3 Best-BlastP=>>nrprot No Hits found

4084.2 Best-BlastP=>>nrprot 55% Identities = 143/383 (37%), Positives = 217/383 (56%), Gaps = 1/383 (0%) ref|ZP_00058706.1| COGG0438: Glycosyltransferase [Thermobifida fusca] Length = 426

4087.2 Best-BlastP=>>nrprot 61% Identities = 175/436 (40%), Positives = 262/436 (60%), Gaps = 25/436 (5%) ref|NP_845547.1| conserved hypothetical protein [Bacillus anthracis str. Ames] gb|AAP27033.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 445

4088.2 Best-BlastP=>>nrprot 75% Identities = 182/288 (63%), Positives = 224/288 (77%) gb|AAM00632.1| unknown [Legionella pneumophila] Length = 294

409.2 Best-BlastP=>>nrprot 56% Identities = 123/352 (34%), Positives = 210/352 (59%), Gaps = 8/352 (2%) ref|NP_820789.1| lipoprotein, putative [Coxiella burnetii RSA 493] gb|AO91303.1| lipoprotein, putative [Coxiella burnetii RSA 493] Length = 391

4093.1 Best-BlastP=> >nrprot 72% Identities = 255/481 (53%), Positives = 346/481 (71%), Gaps = 9/481 (1%) ref|NP_820458.1| glutamyl-tRNA(Gln) amidotransferase, B subunit [Coxiella burnetii RSA 493] Length = 477

4094.2 Best-BlastP=> >nrprot 75% Identities = 284/480 (59%), Positives = 366/480 (76%), Gaps = 1/480 (0%) ref|NP_820457.1| glutamyl-tRNA(Gln) amidotransferase, A subunit [Coxiella burnetii RSA 493] Length = 483

4096.1 Best-BlastP=> >nrprot 70% Identities = 86/155 (55%), Positives = 113/155 (72%) ref|NP_841624.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] ref|NP_841817.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] ref|NP_842206.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] ref|NP_842438.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] ref|NP_842438.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD85496.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD86113.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD86358.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD85700.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] Length = 191

4097.1 Best-BlastP=> >nrprot 62% Identities = 26/34 (76%), Positives = 31/34 (91%) ref|ZP_00111545.1| COG4644: Transposase and inactivated derivatives, TnPA family Length = 1014

4098.1 Best-BlastP=> >nrprot 62% Identities = 33/89 (37%), Positives = 57/89 (64%) gb|AAQ92366.1| transposase [Istotella anguillarum] Length = 980

4101.1 Best-BlastP=> >nrprot 70% Identities = 125/226 (55%), Positives = 166/226 (73%) ref|NP_721272.1| putative ABC transporter, ATP-binding protein [Streptococcus mutans UA159] gb|AAN58578.1|AE014927_7 putative ABC transporter, ATP-binding protein [Streptococcus mutans UA159] Length = 235

4101.1 Best-BlastP=> >nrprot 50% Identities = 22/49 (44%), Positives = 34/49 (69%) ref|NP_277100.1| putative transposase [Deinococcus radiodurans] Length = 828

4104.2 Best-BlastP=> >nrprot 44% Identities = 121/430 (28%), Positives = 195/430 (45%), Gaps = 67/430 (15%) ref|NP_873428.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] gb|AAP955817.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] Length = 481

4105.1 Best-BlastP=> >nrprot 48% Identities = 74/241 (30%), Positives = 126/241 (52%), Gaps = 19/241 (7%) ref|ZP_00132729.1| hypothetical protein [Haemophilus somnus 2336] Length = 270

4106.1 Best-BlastP=> >nrprot 39% Identities = 47/197 (23%), Positives = 88/197 (44%), Gaps = 18/197 (9%) ref|ZP_00123126.1| hypothetical protein [Haemophilus somnus 129P] Length = 212

4107.1 Best-BlastP=> >nrprot No Hits found

4108.1 Best-BlastP=> >nrprot 34% Identities = 61/215 (28%), Positives = 97/215 (45%), Gaps = 29/215 (13%) ref|NP_928397.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE13363.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii TTO1] Length = 245

4109.2 Best-BlastP=>>nrprot 34% Identities = 36/145 (24%), Positives = 67/145 (46%), Gaps = 16/145 (11%) ref|XP_323218.1| hypothetical protein (AL356172) conserved hypothetical protein [Neurospora crassa]) emb|CAD11783.1| conserved hypothetical protein [Neurospora crassa] gb|EA28302.1| hypothetical protein (AL356172) conserved hypothetical protein [Neurospora crassa]) Length = 743

4111.2 Best-BlastP=>>nrprot 97% Identities = 350/359 (97%), Positives = 350/359 (97%), Gaps = 8/359 (2%) emb|CAB65206.1| RmlB protein [Legionella pneumophila] Length = 351

4112.1 Best-BlastP=>>nrprot 99% Identities = 294/294 (100%), Positives = 294/294 (100%) emb|CAB65207.1| RmlD protein [Legionella pneumophila] Length = 294

4113.1 Best-BlastP=>>nrprot 94% Identities = 172/188 (91%), Positives = 177/188 (94%), Gaps = 1/188 (0%) emb|CAB65208.1| RmlC protein [Legionella pneumophila] Length = 188

4115.1 Best-BlastP=>>nrprot 97% Identities = 331/334 (99%), Positives = 332/334 (99%) emb|CAB65212.1| N-acetyleneurameric acid condensing enzyme [Legionella pneumophila] Length = 338

4116.3 Best-BlastP=>>nrprot 99% Identities = 232/232 (100%), Positives = 232/232 (100%) emb|CAB65213.1| CMP-N-acetyleneuramnic acid synthetase [Legionella pneumophila] Length = 232

4118.3 Best-BlastP=>>nrprot 99% Identities = 213/213 (100%), Positives = 213/213 (100%) sp|Q9RDX3|HIS5 LEGPN Imidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH) emb|CAB65214.1| glutamine amidotransferase [Legionella pneumophila] Length = 213

4119.2 Best-BlastP=>>nrprot 82% Identities = 207/210 (98%), Positives = 210/210 (100%) sp|Q9RDX2|HIS6 LEGPN Imidazole glycerol phosphate synthase subunit hisF (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (IGPS subunit hisF) (ImGP synthase subunit hisF) Length = 212

412.3 Best-BlastP=>>nrprot 66% Identities = 189/397 (47%), Positives = 263/397 (66%) ref|NP_820787.1| ABC transporter, permease protein [Coxiella burnetii RSA 493] gb|AAO91301.1| ABC transporter, permease protein [Coxiella burnetii RSA 493] Length = 404

4123.2 Best-BlastP=>>nrprot 63% Identities = 39/74 (52%), Positives = 54/74 (72%), Gaps = 1/74 (1%) gb|AAM08234.1| putative phage repressor [Legionella pneumophila] Length = 227

4126.2 Best-BlastP=>>nrprot 54% Identities = 118/267 (44%), Positives = 164/267 (61%), Gaps = 2/267 (0%) gb|AAM08235.1| LvrA [Legionella pneumophila] Length = 289

4127.1 Best-BlastP=>>nrprot 51% Identities = 47/155 (30%), Positives = 77/155 (49%), Gaps = 20/155 (12%) gb|AAM08236.1| LvrB [Legionella pneumophila] Length = 150

4128.1 Best-BlastP=>>nrprot 61% Identities = 25/62 (40%), Positives = 45/62 (72%), Gaps = 2/62 (3%) emb|CAB60050.1| lvrC [Legionella pneumophila] Length = 67

4129.1 Best-BlastP=>>nrprot 40% Identities = 37/114 (32%), Positives = 62/114 (54%), Gaps = 4/114 (3%) gb|AAL05416.1| PilL [Yersinia pseudotuberculosis] Length = 356

413.5 Best-BlastP=>>nrprot 23% Identities = 104/399 (26%), Positives = 187/399 (46%), Gaps = 28/399 (7%) ref|NP_486788.1| hypothetical protein [Nostoc sp. PCC 7120] p|AE2149 hypothetical protein all2748 [imported] - Nostoc sp. (strain PCC 7120) db|BAB74447.1| ORF_ID:all2748~hypothetical protein [Nostoc sp. PCC 7120] Length = 426

4130.2 Best-BlastP=>>nrprot 45% Identities = 33/104 (31%), Positives = 60/104 (57%), Gaps = 6/104 (5%) ref|NP_819572.1| SMC family protein [Coxiella burnetii RSA 493] emb|CD66594.1| SMC protein [Coxiella burnetii] gb|AAO900086.1| SMC family protein [Coxiella burnetii RSA 493] Length = 1169

4131.3 Best-BlastP=>>nrprot 31% Identities = 60/185 (32%), Positives = 87/185 (47%), Gaps = 8/185 (4%) gb|AAN62293.1|AF440524_80 hypothetical protein [Pseudomonas aeruginosa] Length = 241

4132.3 Best-BlastP=>>nrprot 45% Identities = 42/99 (42%), Positives = 58/99 (58%), Gaps = 2/99 (2%) ref|ZP_00123136.1| hypothetical protein [Haemophilus somnus 129P] Length = 170

4133.1 Best-BlastP=>>nrprot 75% Identities = 39/61 (63%), Positives = 49/61 (80%) ref|NP_403868.1| 50S ribosomal protein L29 [Yersinia pestis] ref|NP_671291.1| 50S ribosomal subunit protein L29 [Yersinia pestis KIM] sp|Q8ZJA4|RL29_YERPE 50S ribosomal protein L29 pir|AB0027 50S ribosomal protein L29 [Imported] - Yersinia pestis (strain CO92) emb|CAC89077.1| 50S ribosomal protein L29 [Yersinia pestis CO92] gb|AM87542.1|AE014002_15 50S ribosomal subunit protein L29 [Yersinia pestis KIM] Length = 63

4134.1 Best-BlastP=>>nrprot 77% Identities = 54/79 (68%), Positives = 66/79 (83%) ref|ZP_00090912.1| COG0186: Ribosomal protein S17 [Azotobacter vinelandii] Length = 90

4135.1 Best-BlastP=>>nrprot 90% Identities = 100/122 (81%), Positives = 110/122 (90%), Gaps = 1/122 (0%) ref|ZP_000067983.1| COG0093: Ribosomal protein L14 [Microbulbifer degradans 240] Length = 122

4136.1 Best-BlastP=>>nrprot 70% Identities = 58/106 (54%), Positives = 77/106 (72%), Gaps = 1/106 (0%) ref|NP_273211.1| 50S ribosomal protein L24 [Neisseria meningitidis MC58] ref|NP_282968.1| 50S ribosomal protein L24 [Neisseria meningitidis Z2491] pir|C81232_50S ribosomal protein L24 NMB0153 [Imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 ribosomal protein L24 [Neisseria meningitidis MC58] emb|CAB83433.1| 50S ribosomal protein L24 [Neisseria meningitidis Z2491] Length = 107

4138.1 Best-BlastP=>>nrprot 83% Identities = 128/178 (71%), Positives = 153/178 (85%) ref|NP_273212.1| 50S ribosomal protein L5 [Neisseria meningitidis MC58] pir|D81232_50S ribosomal protein L5 NMB0154 [Imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF40612.1| 50S ribosomal protein L5 [Neisseria meningitidis MC58] Length = 179

4139.1 Best-BlastP=>>nrprot 65% Identities = 49/101 (48%), Positives = 66/101 (65%), Gaps = 1/101 (0%) ref|ZP_00004335.1| COG0199: Ribosomal protein S14 [Rhodobacter sphaeroides] Length = 101

4140.1 Best-BlastP=>>nrprot 78% Identities = 79/133 (59%), Positives = 103/133 (77%), Gaps = 5/133 (3%) ref|NP_273214.1| 30S ribosomal protein S8 [Neisseria meningitidis MC58] ref|NP_282965.1| 30S ribosomal protein S8 [Neisseria meningitidis Z2491] sp|Q9JF58|RS8_NEIMA_30S ribosomal protein S8 pir|F81232_30S ribosomal protein S8 NMB0156 [Imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) gb|AAF40614.1| 30S ribosomal protein S8 [Neisseria meningitidis MC58] emb|CAB83430.1| 30S ribosomal protein S8 [Neisseria meningitidis Z2491] Length = 130

4141.1 Best-BlastP=>>nrprot 71% Identities = 102/179 (56%), Positives = 129/179 (72%), Gaps = 2/179 (1%) ref|NP_289866.1| 50S ribosomal subunit protein L6 [Escherichia coli O157:H7 EDL933] ref|NP_312197.1| 50S ribosomal subunit protein L6 [Escherichia coli O157:H7] ref|NP_417764.1| 50S ribosomal subunit protein L6 [Escherichia coli K12] ref|NP_709093.1| 50S ribosomal subunit protein L6 [Shigella flexneri 2a str. 301] ref|NP_755932.1| 50S ribosomal protein L6 [Escherichia coli CFT073] ref|NP_839565.1| 50S ribosomal subunit protein L6 [Shigella flexneri 2a str. 2457T] sp|P02390|RL6_ECOLI 50S ribosomal protein L6 pir|R5EC6 ribosomal protein L6 [validated] - cherichia coli (strain K-12) pir|B91150 50S ribosomal subunit protein L6 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) 995 50S ribosomal subunit protein L6 [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gb|AAA58102.1| 50S ribosomal subunit protein L6 [Escherichia coli] gb|AAC76330.1| 50S ribosomal subunit protein L6 [Escherichia coli K12] E005556 19 50S ribosomal subunit protein L6 [Escherichia coli O157:H7 EDL933] dbj|BAB37593.1| 50S ribosomal subunit protein L6 [Escherichia coli O157:H7] E015343_16 50S ribosomal subunit protein L6 [Shigella flexneri 2a str. 301]

4142.3 Best-BlastP=>>nrprot 71% Identities = 65/117 (55%), Positives = 86/117 (73%), Gaps = 4/117 (3%) ref|NP_252937.1| 50S ribosomal protein L18 [Pseudomonas aeruginosa PA01] ref|ZP_00137735.1| COG0256: Ribosomal protein L18 [Pseudomonas aeruginosa UCBPP-PA14] pir|E83114 50S ribosomal protein L18 PA4247 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AGG07635.1|AE004841_13 50S ribosomal protein L18 [Pseudomonas aeruginosa PAO1] Length = 116

4143.3 Best-BlastP=>>nrprot 75% Identities = 105/158 (66%), Positives = 127/158 (80%) ref|ZP_00067978.1| COG0098: Ribosomal protein S5 [Microbulbifer degradans 2-40] Length = 170

4144.3 Best-BlastP=>>nrprot 66% Identities = 31/56 (55%), Positives = 41/56 (73%) ref|NP_56330303.1| 50S ribosomal protein L30 [Clostridium perfringens] dbj|BAB82093.1| 50S ribosomal protein L30 [Clostridium perfringens str. 13] Length = 57

4145.3 Best-BlastP=>>nrprot 76% Identities = 92/144 (63%), Positives = 111/144 (77%) ref|ZP_00067977.1| COG0200: Ribosomal protein L15 [Microbulbifer degradans 2-40] Length = 144

4148.3 Best-BlastP=>>nrprot 81% Identities = 293/437 (67%), Positives = 364/437 (83%) ref|NP_819302.1| preprotein translocase, SecY subunit [Coxiella burnetii RSA 493] gb|AAO89816.1| preprotein translocase, SecY subunit [Coxiella burnetii RSA 493] Length = 442

4149.1 Best-BlastP=>>nrprot 81% Identities = 83/114 (72%), Positives = 97/114 (85%) ref|ZP_00125957.1| COG0099: Ribosomal protein S13 [Pseudomonas syringae pv. syringae B728a] ref|NP_790495.1| ribosomal protein S13 [Pseudomonas syringae pv. tomato str. DC3000] sp|Q889U9|RS13_PSESMM 30S ribosomal protein S13 gb|AAO54190.1| ribosomal protein S13 [Pseudomonas syringae pv. tomato str. DC3000] Length = 118

415.2 Best-BlastP=>>nrprot 57% Identities = 176/280 (62%), Positives = 213/280 (76%), Gaps = 2/280 (0%) ref|NP_838055.1| putative transposase [Shigella flexneri 2a str. 2457T] gb|AAK64580.1| putative transposase [Vibrio cholerae] dbj|BAB79611.1| orf6 [Salmonella enterica subsp. enterica serovar Choleraesuis] gb|AAL59686.1| putative transposase [Vibrio cholerae] gb|AAP17865.1| putative transposase [Shigella flexneri 2a str. 2457T] dbj|BAC79056.1| putative transposase [Vibrio cholerae] Length = 497

4151.1 Best-BlastP=>>nrprot 80% Identities = 91/130 (70%), Positives = 107/130 (82%) ref|NP_660814.1| 30S ribosomal protein S11 [Buchnera aphidicola str. Sg (Schizaphis graminum)] sp|Q8K972|RS11_BUCAP 30S ribosomal protein S11 gb|AAM68025.1| 30S ribosomal protein S11 [Buchnera aphidicola str. Sg (Schizaphis graminum)] Length = 130

4153.1

Best-BlastP=> >nrprot 81% Identities = 139/206 (67%), Positives = 169/206 (82%) ref|NP_289857.1| 30S ribosomal subunit protein S4 [Escherichia coli O157:H7 EDL933] ref|NP_312188.1| 30S ribosomal subunit protein S4 [Escherichia coli O157:H7] ref|NP_417755.1| 30S ribosomal subunit protein S4 [Escherichia coli K12] ref|NP_755921.1| 30S ribosomal protein S4 [Escherichia coli CFT073] 54|RS4_ECOLI_30S ribosomal protein S4 [validated] - Escherichia coli (strain K-12) pir|A91149 30S ribosomal subunit protein S4 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|E85994 30S ribosomal subunit protein S4 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) emb|CAA26394.1| unnamed protein product [Escherichia coli] gb|AAA58094.1| 30S ribosomal subunit protein S4 [Escherichia coli] gb|AAC76321.1| 30S ribosomal subunit protein S4 [Escherichia coli K12] .1|AE005556_10 30S ribosomal subunit protein S4 [Escherichia coli O157:H7 EDL933] dbj|BAB37584.1| 30S ribosomal subunit protein S4 [Escherichia coli_O157:H7] gbl|AN82495.1|AE016767_255 30S ribosomal protein S4 [Escherichia coli CFT073] Length = 206

4154.2 Best-BlastP=> >nrprot 79% Identities = 216/328 (65%), Positives = 264/328 (80%), Gaps = 3/328 (0%) gbl|AAM33636.1|AF506984_1 RpoA [Pseudomonas putida] Length = 333

4156.3 Best-BlastP=> >nrprot 99% Identities = 283/283 (100%), Positives = 283/283 (100%) emb|CAB65193.1| Wzm protein [Legionella pneumophila] Length = 283

4157.2 Best-BlastP=> >nrprot 99% Identities = 473/474 (99%), Positives = 473/474 (99%) emb|CAB65192.1| Wzt protein [Legionella pneumophila] Length = 474

4158.1 Best-BlastP=> >nrprot 98% Identities = 379/382 (99%), Positives = 379/382 (99%) emb|CAB65191.1| hypothetical protein [Legionella pneumophila] Length = 382

4159.1 Best-BlastP=> >nrprot 91% Identities = 273/279 (97%), Positives = 275/279 (98%) emb|CAB65190.1| putative glycosyl transferase [Legionella pneumophila] Length = 297

4160.3 Best-BlastP=> >nrprot 97% Identities = 281/282 (99%), Positives = 281/282 (99%) emb|CAD43478.1| putative glycosyltransferase [Legionella pneumophila] Length = 297

4161.3 Best-BlastP=> >nrprot 99% Identities = 336/339 (99%), Positives = 338/339 (99%) emb|CAB65189.1| putative glycosyl transferase [Legionella pneumophila] Length = 339

4162.2 Best-BlastP=> >nrprot 37% Identities = 188/579 (32%), Positives = 316/579 (54%), Gaps = 35/579 (6%) ref|NP_834965.1| Sensory box/GGDEF family protein [Bacillus cereus ATCC 14579] gbl|AAP12166.1| Sensory box/GGDEF family protein [Bacillus cereus ATCC 14579] Length = 909

4164.1 Best-BlastP=> >nrprot 57% Identities = 138/138 (100%), Positives = 138/138 (100%) gbl|AAD41585.1|AF057704_1 EnhA [Legionella pneumophila] Length = 164

4165.1 Best-BlastP=> >nrprot 68% Identities = 127/133 (95%), Positives = 130/133 (97%) gbl|AAD41586.1|AF057704_2 EnhB [Legionella pneumophila] Length = 142

4167.4 Best-BlastP=> >nrprot 99% Identities = 1193/1201 (99%), Positives = 1198/1201 (99%), Gaps = 1/1201 (0%) gbl|AAD41587.1|AF057704_3 enhanced entry protein EnhC [Legionella pneumophila] Length = 1201

4168.2 Best-BlastP=> >nrprot No Hits found

417.3 Best-BlastP=> >nrprot 30% Identities = 45/190 (23%), Positives = 83/190 (43%), Gaps = 2/190 (1%) ref|ZP_00091084.1| COG0582: Integrase [Azotobacter vinelandii] Length = 287

4170.1 Best-BlastP=>>nrprot 6% Identities = 36/117 (30%), Positives = 57/117 (48%), Gaps = 10/117 (8%) ref|NP_701057.1| hypothetical protein [Plasmodium falciparum 3D7] gb|AAN35781.1|AE014838_59 hypothetical protein [Plasmodium falciparum 3D7] Length = 371

4171.4 Best-BlastP=>>nrprot 52% Identities = 69/147 (46%), Positives = 93/147 (63%), Gaps = 1/147 (0%) ref|ZP_00080184.1| COG1881: Phospholipid-binding protein [Geobacter metallireducens] Length = 176

4172.2 Best-BlastP=>>nrprot 11% Identities = 22/63 (34%), Positives = 39/63 (61%), Gaps = 1/63 (1%) gb|EAA24489.1| hypothetical protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 265

4173.2 Best-BlastP=>>nrprot 62% Identities = 68/129 (52%), Positives = 84/129 (65%), Gaps = 4/129 (3%) ref|NP_230027.1| conserved hypothetical protein [Vibrio cholerae] pir|A82330 conserved hypothetical protein VC0373 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93546.1| conserved hypothetical protein [Vibrio cholerae] Length = 139

4174.1 Best-BlastP=>>nrprot 66% Identities = 57/143 (39%), Positives = 93/143 (65%), Gaps = 7/143 (4%) gb|AAC44222.1| hemin binding protein Hbp [Legionella pneumophila] Length = 141

4175.1 Best-BlastP=>>nrprot 54% Identities = 115/302 (38%), Positives = 169/302 (55%), Gaps = 11/302 (3%) ref|ZP_00086085.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 300

4177.2 Best-BlastP=>>nrprot 13% Identities = 48/172 (27%), Positives = 70/172 (40%), Gaps = 25/172 (14%) dbj|BAC27865.1| unnamed protein product [Mus musculus] Length = 531

4179.2 Best-BlastP=>>nrprot 27% Identities = 86/423 (20%), Positives = 183/423 (43%), Gaps = 69/423 (16%) gb|EAA18183.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 1154

418.4 Best-BlastP=>>nrprot 69% Identities = 119/215 (55%), Positives = 156/215 (72%), Gaps = 3/215 (1%) ref|NP_286845.1| putative carrier/transport protein [Escherichia coli O157:H7] EDL933] ref|NP_309081.1| putative carrier/transport protein [Escherichia coli O157:H7] pir|D85624 probable carrier/transport protein yccA [imported] - Escherichia coli (strain O157:H7, substrate EDL933) pir|F90760 probable carrier/transport protein ECs1054 [imported] - Escherichia putative carrier/transport protein [Escherichia coli O157:H7] EDL933] dbj|BAB34477.1| putative carrier/transport protein [Escherichia coli O157:H7] Length = 219

4181.1 Best-BlastP=>>nrprot No Hits found

4184.1 Best-BlastP=>>nrprot 53% Identities = 34/97 (35%), Positives = 56/97 (57%) ref|NP_820123.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAQ063637.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 106

4186.1 Best-BlastP=>>nrprot 70% Identities = 155/310 (50%), Positives = 210/310 (67%), Gaps = 16/310 (5%) ref|NP_841212.1| Dnaj N-terminal domain:Dnaj C terminal domain [Nitrosomonas europaea ATCC 19718] emb|CAD85066.1| Dnaj N-terminal domain:Dnaj C terminal domain [Nitrosomonas europaea ATCC 19718] Length = 314

4188.1 Best-BlastP=>>nrprot 65% Identities = 171/397 (43%), Positives = 244/397 (61%), Gaps = 36/397 (9%) ref|ZP_00016589.1| hypothetical protein [Rhodospirillum rubrum] Length = 402

419.2 Best-BlastP=>>nrprot 67% Identities = 136/265 (51%), Positives = 182/265 (68%), Gaps = 4/265 (1%) ref|NP_253165.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] pir|E83086 conserved hypothetical protein PA4475 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07863.1|AE004861_4 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 282

4191.1 Best-BlastP=>>nrprot 71% Identities = 258/457 (56%), Positives = 333/457 (72%), Gaps = 3/457 (0%) ref|ZP_00009339.1| hypothetical protein [Rhodopseudomonas palustris] Length = 471

4192.2 Best-BlastP=>>nrprot 66% Identities = 305/605 (50%), Positives = 398/605 (65%), Gaps = 21/605 (3%) ref|ZP_00029131.1| hypothetical protein [Burkholderia fungorum] Length = 642

4194.3 Best-BlastP=>>nrprot 99% Identities = 428/429 (99%), Positives = 428/429 (99%) gbl|AAM00638.1| unknown [Legionella pneumophila] Length = 429

4195.3 Best-BlastP=>>nrprot 46% Identities = 100/388 (25%), Positives = 180/388 (46%), Gaps = 7/388 (1%) ref|NP_820942.1| drug resistance transporter, Bcr/CfIA family [Coxiella burnetii RSA 493] Length = 409

4197.2 Best-BlastP=>>nrprot 91% Identities = 725/730 (99%), Positives = 727/730 (99%) gbl|AAK35045.2|AF330136_1 type II protein secretion LspD [Legionella pneumophila] Length = 730

42.1 Best-BlastP=>>nrprot 98% Identities = 243/250 (97%), Positives = 247/250 (98%) gbl|AAM08246.1| probable conjugal transfer protein [Legionella pneumophila] Length = 250

4200.2 Best-BlastP=>>nrprot No Hits found

4203.2 Best-BlastP=>>nrprot 47% Identities = 121/412 (29%), Positives = 202/412 (49%), Gaps = 29/412 (7%) ref|ZP_00034486.1| COG0642: Signal transduction histidine kinase [Burkholderia fungorum] Length = 479

4205.2 Best-BlastP=>>nrprot No Hits found

4206.2 Best-BlastP=>>nrprot 33% Identities = 156/825 (18%), Positives = 318/825 (38%), Gaps = 118/825 (14%) gbl|EAA20682.1| rhotry protein [Plasmodium yoelii yoelii] Length = 2719

4209.2 Best-BlastP=>>nrprot 42% Identities = 72/314 (22%), Positives = 139/314 (44%), Gaps = 28/314 (8%) gbl|AAB03184.1| TnpA [Pseudomonas putida] Length = 584

421.2 Best-BlastP=>>nrprot 78% Identities = 307/479 (64%), Positives = 377/479 (78%), Gaps = 4/479 (0%) ref|NP_520780.1| PROBABLE TLDD PROTEIN [Ralstonia solanacearum] emb|CAD16366.1| PROBABLE TLDD PROTEIN [Ralstonia solanacearum] Length = 486

4211.2 Best-BlastP=>>nrprot 61% Identities = 182/449 (40%), Positives = 276/449 (61%), Gaps = 11/449 (2%) ref|ZP_00056132.1| COG1355: Predicted dioxygenase [Magnetospirillum magnetotacticum] Length = 468

4212.1 Best-BlastP=>>nrprot 72% Identities = 229/348 (65%), Positives = 263/348 (75%) ref|NP_217654.1| pfIA [Mycobacterium tuberculosis H37Rv] ref|NP_337751.1| pyruvate formate lyase-activating enzyme, putative [Mycobacterium tuberculosis CDC1551] pir|C70646 probable pfIA protein - Mycobacterium tuberculosis (strain H37RV) emb|CAB06292.1| pfA [Mycobacterium tuberculosis H37Rv] gbl|AAK4756.1| pyruvate formate lyase-activating enzyme, putative [Mycobacterium tuberculosis CDC1551] Length = 362

4214.3 Best-BlastP=>>nrprot 54% Identities = 176/517 (34%), Positives = 286/517 (55%), Gaps = 21/517 (4%) ref|NP_790671.1| sensor protein PilS [Pseudomonas syringae pv. tomato str. DC3000] gbl|AAO54366.1| sensor protein PilS [Pseudomonas syringae pv. tomato str. DC3000] Length = 531

422.3 Best-BlastP=>>nrprot 63% Identities = 127/295 (43%) Positives = 187/295 (63%), Gaps = 14/295 (4%) ref|NP_460713.1| putative phosphoesterase [Salmonella typhimurium LT2] gbl|AAL20672.1| putative phosphoesterase [Salmonella typhimurium LT2] Length = 301

4220.2 Best-BlastP=>>nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614_2 unknown [Francisella tularensis subsp. tularensis] Length = 94

4221.3 Best-BlastP=>>nrprot 58% Identities = 38/86 (44%), Positives = 54/86 (62%) dbj|BAC94314.1| acylphosphatase [Vibrio vulnificus YJ016] Length = 90

4222.3 Best-BlastP=>>nrprot 45% Identities = 33/83 (39%), Positives = 48/83 (57%) gb|EAA16908.1| Drosophila melanogaster CG8797 gene product-related [Plasmodium yoelii yoelii] Length = 2198

4225.1 Best-BlastP=>>nrprot No Hits found

4226.2 Best-BlastP=>>nrprot 82% Identities = 578/861 (67%), Positives = 714/861 (82%), Gaps = 5/861 (0%) gb|AAB95117.1| DNA gyrase [Serratia marcescens] Length = 880

4227.1 Best-BlastP=>>nrprot 65% Identities = 238/489 (48%), Positives = 322/489 (65%), Gaps = 4/489 (0%) ref|NP_899921.1| glycerol kinase [Chromobacterium violaceum ATCC 12472] gb|AAQ57930.1| glycerol kinase [Chromobacterium violaceum ATCC 12472] Length = 500

4228.2 Best-BlastP=>>nrprot 64% Identities = 229/504 (45%), Positives = 327/504 (64%), Gaps = 15/504 (2%) ref|ZP_00091277.1| COG0578: Glycerol-3-phosphate dehydrogenase [Azotobacter vinelandii] Length = 510

423.2 Best-BlastP=>>nrprot 47% Identities = 139/430 (32%), Positives = 204/430 (47%), Gaps = 28/430 (6%) ref|NP_407457.1| hypothetical protein [Yersinia pestis] pir|AD0489 hypothetical protein YPO4021 [imported] - Yersinia pestis (strain CO92) emb|CAC93480.1| hypothetical protein [Yersinia pestis CO92] Length = 414

4231.2 Best-BlastP=>>nrprot 16% Identities = 49/205 (23%), Positives = 81/205 (39%), Gaps = 31/205 (15%) emb|CAE02991.1| OSJNBA0043L09.10 [Oryza sativa (japonica cultivar-group)] Length = 687

4232.3 Best-BlastP=>>nrprot 42% Identities = 73/161 (45%), Positives = 103/161 (63%), Gaps = 1/161 (0%) ref|ZP_00088088.1| COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Pseudomonas fluorescens PfO-1] Length = 241

4233.3 Best-BlastP=>>nrprot No Hits found

4234.3 Best-BlastP=>>nrprot No Hits found

4236.3 Best-BlastP=>>nrprot 58% Identities = 257/678 (37%), Positives = 391/678 (57%), Gaps = 37/678 (5%) ref|ZP_00087890.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 701

4238.1 Best-BlastP=>>nrprot No Hits found

4239.4 Best-BlastP=>>nrprot No Hits found

424.1 Best-BlastP=>>nrprot 73% Identities = 63/103 (61%), Positives = 76/103 (73%) ref|ZP_00082900.1| COG0662: Mannose-6-phosphate isomerase [Pseudomonas fluorescens PfO-1] Length = 103

4242.2 Best-BlastP=>>nrprot 34% Identities = 67/250 (26%), Positives = 112/250 (44%), Gaps = 18/250 (7%) ref|XP_340725.1| iron/ascorbate oxidoreductase family protein, putative [Trypanosoma brucei] gb|AAQ16084.1| iron/ascorbate oxidoreductase family protein, putative [Trypanosoma brucei] Length = 319

4243.2 Best-BlastP=>>nrprot 67% Identities = 76/154 (49%), Positives = 101/154 (65%), Gaps = 8/154 (5%) ref|NP_360925.1| unknown [Rickettsia conorii] pir|H97860 hypothetical protein RC1288 [imported] - Rickettsia conorii (strain Malish 7) gb|AAI03826.1| unknown [Rickettsia conorii] Length = 154

4244.1 Best-BlastP=>>nrprot No Hits found

4246.2 Best-BlastP=>>nrprot 54% Identities = 95/280 (33%), Positives = 154/280 (55%), Gaps = 7/280 (2%) gb|AAM73852.1|AF454863_1 putative lipase LipA [Legionella pneumophila] Length = 282

4247.2 Best-BlastP=>>nrprot 40% Identities = 63/264 (23%), Positives = 117/264 (44%), Gaps = 9/264 (3%) ref|ZP_00118032.1| COG1560: Lauroyl/myristoyl acyltransferase [Cytophaga hutchinsonii] Length = 307

4248.1 Best-BlastP=>>nrprot 52% Identities = 31/74 (41%), Positives = 47/74 (63%), Gaps = 6/74 (8%) ref|ZP_00066809.1| COG1748: Saccharopine dehydrogenase and related proteins [Microbulbifer degradans 2-40] Length = 371

4249.1 Best-BlastP=>>nrprot 36% Identities = 89/354 (25%), Positives = 144/354 (40%), Gaps = 39/354 (11%) gb|EAA22829.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 2694

425.1 Best-BlastP=>>nrprot No Hits found

4250.1 Best-BlastP=>>nrprot No Hits found

4251.2 Best-BlastP=>>nrprot No Hits found

4253.1 Best-BlastP=>>nrprot 55% Identities = 173/457 (37%), Positives = 272/457 (59%), Gaps = 19/457 (4%) ref|NP_654426.1| aa_permeases, Amino acid permease [Bacillus anthracis A2012] ref|NP_843029.1| amino acid permease family protein [Bacillus anthracis str. Ames] gb|AAP24515.1| amino acid permease family protein [Bacillus anthracis str. Ames] Length = 473

4254.2 Best-BlastP=>>nrprot No Hits found

4255.1 Best-BlastP=>>nrprot No Hits found

4259.2 Best-BlastP=>>nrprot 57% Identities = 104/292 (35%), Positives = 167/292 (57%), Gaps = 31/292 (10%) ref|ZP_00065076.1| COG1766: Flagellar biosynthesis/type III secretory pathway lipoprotein [Microbulbifer degradans 2-40] Length = 556

426.3 Best-BlastP=>>nrprot No Hits found

4262.2 Best-BlastP=>>nrprot 47% Identities = 42/141 (29%), Positives = 72/141 (51%) ref|NP_249796.1| flagellar protein FlJ [Pseudomonas aeruginosa PA01] ref|ZP_00138693.1| COG2882: Flagellar biosynthesis chaperone [Pseudomonas aeruginosa (strain PAO1) gb|AAG04494.1|AE004540_14 flagellar protein FlJ [Pseudomonas aeruginosa PAO1] Length = 147

4266.3 Best-BlastP=>>nrprot 35% Identities = 82/312 (26%), Positives = 145/312 (46%), Gaps = 51/312 (16%) gb|AAN63820.1| lysophospholipase A [Legionella pneumophila] Length = 309

4267.5 Best-BlastP=>>nrprot 68% Identities = 360/694 (51%), Positives = 475/694 (68%), Gaps = 15/694 (2%) emb|CAA86935.1| polyphosphate kinase [Acinetobacter sp. ADP1] Length = 691

4269.3 Best-BlastP=>>nrprot No Hits found

427.3 Best-BlastP=>>nrprot 67% Identities = 127/239 (53%), Positives = 174/239 (72%), Gaps = 5/239 (2%) ref|NP_743000.1| RNA methyltransferase, TrmH family, group 1 [Pseudomonas putida KT2440] gb|AAN66464.1|AE016275_9 RNA methyltransferase, TrmH family, group 1 [Pseudomonas putida KT2440] Length = 251

4272.3 Best-BlastP=>>nrprot No Hits found

4273.1 Best-BlastP=>>nrprot 35% Identities = 83/286 (29%), Positives = 133/286 (46%), Gaps = 2/286 (0%) ref|ZP_00065171.1| COG0583: Transcriptional regulator [Microbulbifer degradans 2-40] Length = 299

4275.2 Best-BlastP=> >nrprot 49% Identities = 77/244 (31%), Positives = 120/244 (49%), Gaps = 19/244 (7%) ref|NP_661075.1| oxidoreductase, short-chain dehydrogenase/reductase family [Chlorobium tepidum TLS] gb|AAM71417.1| oxidoreductase, short-chain dehydrogenase/reductase family Length = 246

4276.2 Best-BlastP=> >nrprot 11% Identities = 46/1172 (26%), Positives = 73/1172 (42%), Gaps = 36/1172 (20%) dbj|BAC96628.1| conserved hypothetical protein [Vibrio vulnificus YJ016] Length = 442

428.1 Best-BlastP=> >nrprot 75% Identities = 142/257 (55%), Positives = 197/257 (76%) ref|NP_820132.1| inositol-1-monophosphatase [Coxiella burnetii RSA 493] gb|AAO90646.1| inositol-1-monophosphatase [Coxiella burnetii RSA 493] Length = 266

4281.2 Best-BlastP=> >nrprot 50% Identities = 32/88 (36%), Positives = 45/88 (51%), Gaps = 4/88 (4%) ref|NP_441652.1| unknown protein [Synechocystis sp. PCC 6803] pirl|S75873 hypothetical protein srl1163 - Synechocystis sp. (strain PCC 6803) dbj|BAA18332.1| ORF_ID.srl1163~unknown protein [Synechocystis sp. PCC 6803] Length = 556

4282.2 Best-BlastP=> >nrprot 67% Identities = 126/249 (50%), Positives = 169/249 (67%), Gaps = 2/249 (0%) gb|AAM51645.1| putative transposase [Francisella tularensis subsp. tularensis] Length = 247

4284.2 Best-BlastP=> >nrprot 41% Identities = 100/266 (37%), Positives = 142/266 (53%), Gaps = 35/266 (13%) ref|NP_769986.1| bli3346 [Bradyrhizobium japonicum] dbj|BAC48611.1| bli3346 [Bradyrhizobium japonicum USDA 110] Length = 314

4285.1 Best-BlastP=> >nrprot No Hits found

4288.2 Best-BlastP=> >nrprot 98% Identities = 314/322 (97%), Positives = 318/322 (98%) gb|AAD43224.1|AF111940_6 LspK precursor [Legionella pneumophila] Length = 322

4289.2 Best-BlastP=> >nrprot 99% Identities = 203/205 (99%), Positives = 204/205 (99%) gb|AAD43223.1|AF111940_5 LspJ precursor [Legionella pneumophila] Length = 205

429.2 Best-BlastP=> >nrprot 60% Identities = 149/315 (47%), Positives = 207/315 (65%), Gaps = 4/315 (1%) ref|NP_793611.1| signal peptide peptidase SppA, 36K type peptidase SppA, 36K type [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57306.1| signal peptide peptidase SppA, 36K type [Pseudomonas syringae pv. tomato str. DC3000] Length = 332

4291.1 Best-BlastP=> >nrprot 98% Identities = 123/125 (98%), Positives = 124/125 (99%) gb|AAD43222.1|AF111940_4 Lsp precursor [Legionella pneumophila] Length = 125

4293.2 Best-BlastP=> >nrprot 67% Identities = 116/253 (45%), Positives = 173/253 (68%), Gaps = 1/253 (0%) ref|NP_927916.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTC1] emb|CAE12861.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii TTC1] Length = 258

4294.3 Best-BlastP=> >nrprot 57% Identities = 107/276 (38%), Positives = 161/276 (58%) ref|NP_720100.1| cell division ABC transporter, permease protein FtsX [Shewanella oneidensis MR-1] onedensis MR-1 Length = 321

4295.3 Best-BlastP=> >nrprot 69% Identities = 210/424 (49%), Positives = 301/424 (70%) ref|NP_820879.1| peptidase, M16 family [Coxiella burnetii RSA 493] gb|AAO91393.1| peptidase, M16 family [Coxiella burnetii RSA 493] Length = 459

4296.1 Best-BlastP=> >nrprot 63% Identities = 164/388 (42%), Positives = 248/388 (63%) ref|NP_820878.1| peptidase, M16 family [Coxiella burnetii RSA 493] gb|AAO91392.1| peptidase, M16 family [Coxiella burnetii RSA 493] Length = 443

4297.2 Best-BlastP=> >nrprot 64% Identities = 85/182 (46%), Positives = 117/182 (64%), Gaps = 6/182 (3%) ref|ZP_00134417.1| COG0742: N6-adenine-specific methylase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] pleuropneumoniae serovar 1 str. 4074 Length = 197

43.1 Best-BlastP=>>nrprot 97% Identities = 228/238 (95%), Positives = 233/238 (97%) gb|AAM08245.1| probable conjugal transfer protein [Legionella pneumophila] Length = 238

4301.1 Best-BlastP=>>nrprot 63% Identities = 130/287 (45%), Positives = 188/287 (65%), Gaps = 2/287 (0%) ref|XP_306575.1| ENSANGP0000014633 [Anopheles gambiae] gb|EAA02168.1| ENSANGP0000014633 [Anopheles gambiae str. PEST] Length = 304

4302.1 Best-BlastP=>>nrprot 81% Identities = 190/271 (70%), Positives = 227/271 (83%) ref|NP_459218.1| 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [Salmonella typhimurium LT2] Length = 274

4303.1 Best-BlastP=>>nrprot 68% Identities = 203/374 (54%), Positives = 258/374 (68%), Gaps = 1/374 (0%) ref|ZP_00064957.1| COG0624: Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases [Microbacterium degradans 2-40] Length = 382

4305.2 Best-BlastP=>>nrprot No Hits found

4307.2 Best-BlastP=>>nrprot No Hits found

4309.2 Best-BlastP=>>nrprot 37% Identities = 79/320 (24%), Positives = 143/320 (44%), Gaps = 16/320 (5%) gb|AAC83363.1| outer membrane secretion protein Y [Pseudomonas alcaligenes] Length = 381

431.1 Best-BlastP=>>nrprot No Hits found

4310.1 Best-BlastP=>>nrprot 45% Identities = 34/139 (24%), Positives = 71/139 (51%), Gaps = 3/139 (2%) ref|NP_755574.1| Putative general secretion pathway protein M-type yghD [Escherichia coli CFT073] gb|AAN82147.1|AE016766_235 Putative general secretion pathway protein M-type yghD [Escherichia coli CFT073] Length = 178

4311.1 Best-BlastP=>>nrprot 41% Identities = 47/173 (27%), Positives = 74/173 (42%), Gaps = 14/173 (8%) ref|NP_232963.1| DamX-related protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82443 DamX-related protein VCA0573 [imported] - Vibrio cholerae (strain N16961) Length = 195

4312.2 Best-BlastP=>>nrprot 57% Identities = 186/432 (43%), Positives = 253/432 (58%), Gaps = 8/432 (1%) ref|NP_231613.1| deoxyguanosinetriphosphate triphosphohydrolase [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KQL9|DG1A_VIBCH Deoxyguanosinetriphosphate triphosphohydrolase-like protein 1 pir|B82132 deoxyguanosinetriphosphate triphosphohydrolase VC1979 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95127.1| deoxyguanosinetriphosphate triphosphohydrolase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 441

4316.4 Best-BlastP=>>nrprot 23% Identities = 87/391 (22%), Positives = 154/391 (39%), Gaps = 61/391 (15%) gb|AAC21558.1| paramyosin related protein [Echinococcus granulosus] Length = 601

4319.2 Best-BlastP=>>nrprot 38% Identities = 56/226 (24%), Positives = 95/226 (42%), Gaps = 24/226 (10%) ref|NP_820254.1| ompA-like transmembrane domain protein [Coxiella burnetii RSA 493] gb|AO90768.1| ompA-like transmembrane domain protein [Coxiella burnetii RSA 493] Length = 248

432.1 Best-BlastP=>>nrprot No Hits found

4320.1 Best-BlastP=> >nrprot 61% Identities = 163/420 (38%), Positives = 265/420 (63%), Gaps = 4/420 (0%) ref|NP_249285.1| peptidyl-prolyl cis-trans isomerase SurA [Pseudomonas aeruginosa PA01] pir||B83572 peptidyl-prolyl cis-trans isomerase SurA PA0594 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG03983.1| IAE004495_7 peptidyl-prolyl cis-trans isomerase SurA [Pseudomonas aeruginosa PAO1] Length = 430

4321.2 Best-BlastP=> >nrprot 48% Identities = 274/816 (33%), Positives = 410/816 (50%), Gaps = 61/816 (7%) ref|NP_820953.1| organic solvent tolerance protein [Coxiella burnetii RSA 493] gb|AAO91467.1| organic solvent tolerance protein [Coxiella burnetii RSA 493] Length = 870

4322.1 Best-BlastP=> >nrprot 57% Identities = 133/323 (41%), Positives = 187/323 (57%), Gaps = 9/323 (2%) ref|NP_840285.1| Domain of unknown function DUF227 [Nitrosomonas europaea ATCC 19718] emb|CAD84102.1| Domain of unknown function DUF227 [Nitrosomonas europaea ATCC 19718] Length = 332

4323.1 Best-BlastP=> >nrprot 65% Identities = 105/218 (48%), Positives = 145/218 (66%), Gaps = 4/218 (1%) ref|ZP_00126866.1| COG1208: Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon) [Pseudomonas syringae pv. syringae B728a] Length = 223

4325.3 Best-BlastP=> >nrprot 66% Identities = 154/307 (50%), Positives = 205/307 (66%), Gaps = 1/307 (0%) ref|NP_462824.1| porphobilinogen deaminase (hydroxymethylbilane synthase) [Salmonella typhimurium LT2] gb|AAF33453.1| 89% identity with E. coli porphobilinogen deaminase (HEMC) (SP:P06983); contains similarity to Pfam family PF01379 (Porphobilinogen deaminase), score=627.8, E=6.2e-185, N=1 [Salmonella typhimurium LT2] gb|AAI22783.1| porphobilinogen deaminase [Salmonella typhimurium LT2] Length = 318

4326.1 Best-BlastP=> >nrprot 50% Identities = 75/233 (32%), Positives = 127/233 (54%), Gaps = 3/233 (1%) dbj|BAC92844.1| uroporphyrinogen-III synthase [Vibrio vulnificus YJ016] Length = 260

4327.1 Best-BlastP=> >nrprot 40% Identities = 86/318 (27%), Positives = 151/318 (47%), Gaps = 26/318 (8%) ref|ZP_00065835.1| COG2959: Uncharacterized enzyme of heme biosynthesis [Microbulbifer degradans 2-40] Length = 494

4328.1 Best-BlastP=> >nrprot 56% Identities = 139/389 (35%), Positives = 224/389 (57%), Gaps = 3/389 (0%) ref|NP_821051.1| hemY protein [Coxiella burnetii RSA 493] gb|AAO91565.1| hemY protein [Coxiella burnetii RSA 493] Length = 392

433.1 Best-BlastP=> >nrprot 99% Identities = 1007/1009 (99%), Positives = 1008/1009 (99%) pir||T18339 icmB protein - Legionella pneumophila emb|CAA75170.1| icmB protein [Legionella pneumophila] gb|AAC38183.1| Dto [Legionella pneumophila] emb|CAA75336.1| icmB protein [Legionella pneumophila] Length = 1009

4332.1 Best-BlastP=> >nrprot 59% Identities = 82/151 (54%), Positives = 107/151 (70%) ref|ZP_00024252.1| COG0412: Dienelactone hydrolase and related enzymes [Ralstonia metallidurans] Length = 435

4333.1 Best-BlastP=> >nrprot 61% Identities = 128/282 (45%), Positives = 174/282 (61%), Gaps = 4/282 (1%) ref|ZP_00077190.1| COG0454: Histone acetyltransferases [Methanoscarcina barkeri] Length = 286

4334.1 Best-BlastP=> >nrprot 62% Identities = 135/293 (46%), Positives = 187/293 (63%), Gaps = 6/293 (2%) ref|NP_421406.1| conserved hypothetical protein [Caulobacter crescentus CB15] pir||B87572 conserved hypothetical protein CC2605 [imported] - Caulobacter crescentus gb|AAK24574.1| conserved hypothetical protein [Caulobacter crescentus CB15] Length = 304

4336.2 Best-BlastP=>>nrprot 59% Identities = 163/401 (40%), Positives = 242/401 (60%), Gaps = 1/401 (0%) ref|NP_626512.1| putative integral membrane protein. [Streptomyces coelicolor A3(2)] pir|T50573 probable integral membrane protein [imported] - Streptomyces coelicolor emb|CAB61710.1| putative integral membrane protein. [Streptomyces coelicolor A3(2)] Length = 431

4337.3 Best-BlastP=>>nrprot 57% Identities = 36/63 (57%), Positives = 48/63 (76%), Gaps = 2/63 (3%) ref|NP_799393.1| putative signal peptide protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61277.1| putative signal peptide protein [Vibrio parahaemolyticus] Length = 86

4338.3 Best-BlastP=>>nrprot 68% Identities = 147/290 (50%), Positives = 206/290 (71%), Gaps = 1/290 (0%) ref|NP_781198.1| myo-inositol catabolism protein iolE [Clostridium tetani E88] gbl|AAO35135.1| myo-inositol catabolism protein iolE [Clostridium tetani E88] Length = 298

4339.1 Best-BlastP=>>nrprot 72% Identities = 347/644 (53%), Positives = 451/644 (70%), Gaps = 25/644 (3%) ref|ZP_00131855.1| COG3962: Acetolactate synthase [Haemophilus somnus 2336] Length = 645

434.3 Best-BlastP=>>nrprot 99% Identities = 207/208 (99%), Positives = 207/208 (99%) pir|T18338 icmJ protein - Legionella pneumophila emb|CAA75169.1| icmJ protein [Legionella pneumophila] gbl|AAC38184.1| DntN [Legionella pneumophila] emb|CAA75335.1| icmJ protein [Legionella pneumophila] Length = 208

4340.2 Best-BlastP=>>nrprot 36% Identities = 179/356 (50%), Positives = 232/356 (65%), Gaps = 4/356 (1%) ref|ZP_00122182.1| COG3892: Uncharacterized protein conserved in bacteria [Haemophilus somnus 129PT] Length = 636

4341.3 Best-BlastP=>>nrprot No Hits found

4342.1 Best-BlastP=>>nrprot 53% Identities = 29/77 (37%), Positives = 44/77 (57%) ref|NP_289764.1| orf, hypothetical protein [Escherichia coli O157:H7 EDL933] ref|NP_312096.1| hypothetical protein [Escherichia coli O157:H7] ref|NP_417657.1| hypothetical protein [Escherichia coli K12] ref|NP_708989.1| orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref|NP_755814.1| Protein yrbA [Escherichia coli CFT073] ref|NP_838699.1| hypothetical protein [Shigella flexneri 2a str. 2457T] pir|H65109 hypothetical 9.5 kD protein in murZ-rpN intergenic region - Escherichia coli (strain K-12) pir|E91137 hypothetical protein ECs4069 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|H85982 hypothetical protein yrbA [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gbl|AAA57991.1| ORF_f89 [Escherichia coli] gbl|AAC76222.1| orf, hypothetical protein [Shigella flexneri 2a str. 301] gbl|AAF21251.1|AF053073_4 YrbA [Shigella flexneri] gbl|AGG58324.1|AE005547_10 orf, hypothetical protein [Escherichia coli K12] gbl|BAB37492.1| hypothetical protein [Escherichia coli O157:H7] gbl|AN44696.1|AE015334_10 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] gbl|AN82388.1|AE016767_148 F

4344.1 Best-BlastP=>>nrprot 80% Identities = 272/419 (64%), Positives = 339/419 (80%) ref|NP_794195.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000] gbl|AAO57890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000] Length = 421

4345.1 Best-BlastP=>>nrprot 71% Identities = 136/252 (53%), Positives = 182/252 (72%), Gaps = 3/252 (1%) ref|NP_718206.1| conserved hypothetical protein TIGR00486 [Shewanella oneidensis MR-1] gbl|AN55650.1|AE015704_1 conserved hypothetical protein TIGR00486 [Shewanella oneidensis MR-1] Length = 250

4346.2 Best-BlastP=>>nrprot 71% Identities = 153/286 (53%), Positives = 207/286 (72%), Gaps = 1/286 (0%) ref|NP_249701.1| dihydropicolinic acid synthase [Pseudomonas aeruginosa PA01] spj|Q914W3|DAPA_PSEAE Dihydropicolinic acid synthase (DHDPS) pir|C83520 dihydropicolinic acid synthase PA1010 [imported] - Pseudomonas aeruginosa (strain PAO1) gbl|AAG04399.1|AE004533_10 dihydropicolinic acid synthase [Pseudomonas aeruginosa PAO1] Length = 292

4347.2 Best-BlastP=>>nrprot 44% Identities = 31/68 (45%), Positives = 38/68 (55%), Gaps = 7/68 (10%) ref[ZP_00035058.1| COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Burkholderia fungorum] Length = 237

4349.2 Best-BlastP=>>nrprot 81% Identities = 180/260 (69%), Positives = 213/260 (81%) ref[NP_900365.1| 3-hydroxybutyrate dehydrogenase [Chromobacterium violaceum ATCC 12472] gb|AAQ58371.1| 3-hydroxybutyrate dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 260

4350.2 Best-BlastP=>>nrprot 59% Identities = 152/375 (40%), Positives = 230/375 (61%), Gaps = 4/375 (1%) ref[ZP_00008996.1| COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Rhodopseudomonas palustris] Length = 379

4351.2 Best-BlastP=>>nrprot 73% Identities = 161/286 (56%), Positives = 221/286 (77%) ref[NP_522970.1| PROBABLE CHEMOTAXIS (MOTILITY solanacearum) emb|CAD18562.1| PROBABLE CHEMOTAXIS (MOTILITY PROTEIN A) PROTEIN A) TRANSMEMBRANE [Ralstonia solanacearum] Length = 286

4352.3 Best-BlastP=>>nrprot 61% Identities = 140/284 (49%), Positives = 191/284 (67%), Gaps = 1/284 (0%) ref[NP_840146.1| Bacterial outer membrane protein [Nitrosomonas europaea ATCC 19718] emb|CAD83956.1| Bacterial outer membrane protein [Nitrosomonas europaea ATCC 19718] Length = 307

4353.2 Best-BlastP=>>nrprot No Hits found

4354.2 Best-BlastP=>>nrprot No Hits found

4355.2 Best-BlastP=>>nrprot 64% Identities = 161/310 (51%), Positives = 204/310 (65%), Gaps = 5/310 (1%) ref[NP_438574.1| hypothetical protein [Haemophilus influenzae Rd] sp|P44433|RLUC_HAEIN Ribosomal large subunit pseudouridine synthase C (Pseudouridylate synthase) (Uracil hydrolase) pir|G64151 hypothetical protein H0412 - Haemophilus influenzae (strain Rd) Length = 322 hypothetical protein [Haemophilus influenzae Rd] Length = 322

4356.2 Best-BlastP=>>nrprot 52% Identities = 77/215 (35%), Positives = 116/215 (53%), Gaps = 8/215 (3%) ref[ZP_00013688.1| hypothetical protein [Rhodospirillum rubrum] Length = 236

4357.3 Best-BlastP=>>nrprot 98% Identities = 414/424 (97%), Positives = 420/424 (99%) gb|AAM00604.1| putative histidine kinase [Legionella pneumophila] Length = 424

4358.2 Best-BlastP=>>nrprot 49% Identities = 64/187 (34%), Positives = 91/187 (48%), Gaps = 7/187 (3%) ref[NP_761114.1| Guanylate cyclase-related protein [Vibrio vulnificus CMCP6] gb|AAO10641.1|AE016804_151 Guanylate cyclase-related protein [Vibrio vulnificus CMCP6] dbj|BAC94846.1| guanylate cyclase-related protein [Vibrio vulnificus YJ016] Length = 185

436.4 Best-BlastP=>>nrprot No Hits found

4363.2 Best-BlastP=>>nrprot 43% Identities = 68/183 (37%), Positives = 106/183 (57%), Gaps = 2/183 (1%) ref[ZP_00073054.1| COG3555: Aspartyl/asparaginyl beta-hydroxylase and related dioxygenases [Trichodesmium erythraeum MS101] Length = 283

4364.2 Best-BlastP=>>nrprot 41% Identities = 36/77 (46%), Positives = 44/77 (57%) pir|D72548 hypothetical protein APE1672 - Aeropyrum permix (strain K1) dbj|BAA80673.1| 113aa long hypothetical protein [Aeropyrum permix] Length = 113

4365.4 Best-BlastP=>>nrprot 63% Identities = 78/175 (44%), Positives = 115/175 (65%), Gaps = 6/175 (3%) ref[ZP_00021197.1| COG0262: Dihydrofolate reductase [Ralstonia metallidurans] Length = 177

4366.1 Best-BlastP=>>nrprot 47% Identities = 37/123 (30%), Positives = 66/123 (53%), Gaps = 4/123 (3%) ref[NP_800262.1| glutathione S-transferase-related protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62095.1| glutathione S-transferase-related protein [Vibrio parahaemolyticus] Length = 128

4367.1 Best-BlastP=>>nrprot No Hits found
 4369.1 Best-BlastP=>>nrprot 35% Identities = 53/153 (34%), Positives = 79/153 (51%), Gaps = 2/153 (1%) ref|ZP_00026335.1| COG3714: Predicted membrane protein [Ralstonia metallidurans] Length = 233

4370.1 Best-BlastP=>>nrprot No Hits found
 4371.1 Best-BlastP=>>nrprot 57% Identities = 122/252 (48%), Positives = 171/252 (67%), Gaps = 4/252 (1%) ref|NP_819457.1| polysaccharide deacetylase-related protein [Coxiella burnetii RSA 493] Length = 276

4372.3 Best-BlastP=>>nrprot 61% Identities = 167/391 (42%), Positives = 247/391 (63%), Gaps = 5/391 (1%) ref|NP_820110.1| membrane-bound lytic murein transglycosylase family protein [Coxiella burnetii RSA 493] gbl|AAO90624.1| membrane-bound lytic murein transglycosylase family protein [Coxiella burnetii RSA 493] Length = 400

4373.3 Best-BlastP=>>nrprot 64% Identities = 45/105 (42%), Positives = 68/105 (64%), Gaps = 7/105 (6%) ref|NP_800642.1| hypothetical protein VPA1132 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62475.1| hypothetical protein [Vibrio parahaemolyticus] Length = 108

4374.4 Best-BlastP=>>nrprot 68% Identities = 262/502 (52%), Positives = 358/502 (71%) ref|NP_819429.1| integral membrane protein MvIN [Coxiella burnetii RSA 493] gbl|AAO89943.1| integral membrane protein MvIN [Coxiella burnetii RSA 493] Length = 515

4376.3 Best-BlastP=>>nrprot 63% Identities = 105/215 (48%), Positives = 143/215 (66%) pdb|1AZQ| Dna Mismatch Repair Protein Mutu From E. Coli Length = 232

4377.4 Best-BlastP=>>nrprot No Hits found
 4378.2 Best-BlastP=>>nrprot 75% Identities = 135/205 (65%), Positives = 167/205 (81%), Gaps = 1/205 (0%) ref|NP_799538.1| antibiotic acetyltransferase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61371.1| antibiotic acetyltransferase [Vibrio parahaemolyticus] Length = 212

4379.1 Best-BlastP=>>nrprot 40% Identities = 85/221 (38%), Positives = 120/221 (54%), Gaps = 8/221 (3%) ref|ZP_00108724.1| COG3393: Predicted acetyltransferase [Nostoc punctiforme] Length = 222

4381.2 Best-BlastP=>>nrprot 79% Identities = 276/420 (65%), Positives = 340/420 (80%) ref|NP_819962.1| amino acid permease family protein [Coxiella burnetii RSA 493] gbl|AAO90476.1| amino acid permease family protein [Coxiella burnetii RSA 493] Length = 437

4383.2 Best-BlastP=>>nrprot 37% Identities = 83/190 (43%), Positives = 109/190 (57%), Gaps = 3/190 (1%) ref|NP_435788.1| hypothetical protein [Sinorhizobium meliloti] pir|F95329 hypothetical protein Sma1005 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA gbl|AAK65200.1| hypothetical protein [Sinorhizobium meliloti] Length = 266

4384.2 Best-BlastP=>>nrprot 55% Identities = 171/477 (35%), Positives = 267/477 (55%), Gaps = 9/477 (1%) ref|NP_819538.1| proton/peptide symporter family protein [Coxiella burnetii RSA 493] gbl|AAO90052.1| proton/peptide symporter family protein [Coxiella burnetii RSA 493] Length = 492

4385.1 Best-BlastP=>>nrprot 85% Identities = 411/546 (75%), Positives = 474/546 (86%), Gaps = 3/546 (0%) ref|NP_230848.1| urocanate hydrolase [Vibrio cholerae O1 biovar eltor str. N16961] sptQ9KSQ3|HUTU_VIBCH Urocanate hydrolase (Urocanase) (Imidazolonepropionate hydrolase) pir|F82228 urocanate hydrolase VC1203 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gbl|AAF94362.1| urocanate hydrolase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 565

4386.2 Best-BlastP=> >nrprot 73% Identities = 296/486 (60%), Positives = 375/486 (77%), Gaps = 1/486 (0%) ref|NP_230847.1| histidine ammonia-lyase [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KSQ4|HUTH_VIBCH Histidine ammonia-lyase (Histidase) pir|E82228 histidine ammonia-lyase (EC 4.3.1.3) [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1) gb|AAF94361.1| histidine ammonia-lyase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 511

4387.3 Best-BlastP=> >nrprot 62% Identities = 96/190 (50%), Positives = 128/190 (67%), Gaps = 1/190 (0%) ref|NP_246159.1| Dam [Pasteurella multocida] gb|AAK03306.1| Dam [Pasteurella multocida] gb|AAL05884.1|AF411317_2 DNA adenine methylase [Pasteurella multocida] Length = 301

4388.1 Best-BlastP=> >nrprot 54% Identities = 151/402 (37%), Positives = 232/402 (57%), Gaps = 5/402 (1%) ref|NP_819596.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO90110.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 421

4389.2 Best-BlastP=> >nrprot 62% Identities = 206/405 (50%), Positives = 270/405 (66%), Gaps = 8/405 (1%) ref|NP_820255.1| D-alanyl-D-alanine carboxypeptidase [Coxiella burnetii RSA 493] gb|AAO90769.1| D-alanyl-D-alanine carboxypeptidase [Coxiella burnetii RSA 493] Length = 418

4391.1 Best-BlastP=> >nrprot 98% Identities = 270/278 (97%), Positives = 275/278 (98%) emb|CAD90964.1| putative D-Ala-amino transferase [Legionella pneumophila] Length = 278

4392.1 Best-BlastP=> >nrprot 60% Identities = 35/87 (40%), Positives = 53/87 (60%) ref|NP_841528.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] sp|Q82UJ7|YE87_NITEU Hypothetical UPF0250 protein NE1487 emb|CAD85398.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 87

4393.1 Best-BlastP=> >nrprot 98% Identities = 192/199 (96%), Positives = 196/199 (98%) emb|CAD90955.1| LssX protein [Legionella pneumophila] Length = 199

4394.4 Best-BlastP=> >nrprot 98% Identities = 666/678 (98%), Positives = 672/678 (99%) emb|CAD90962.1| LssY protein [Legionella pneumophila] Length = 678

4395.2 Best-BlastP=> >nrprot 63% Identities = 337/723 (46%), Positives = 453/723 (62%), Gaps = 27/723 (3%) ref|NP_251738.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] pir|A83266 conserved hypothetical protein PA3048 [imported] - *Pseudomonas aeruginosa* (strain PA01) gb|AAG06436.1|AE004729_10 conserved hypothetical protein [Pseudomonas aeruginosa PA01] Length = 725

4396.1 Best-BlastP=> >nrprot 59% Identities = 66/157 (42%), Positives = 95/157 (60%) ref|ZP_00090069.1| COG3028: Undecharacterized protein conserved in bacteria [Azotobacter vinelandii] Length = 172

4398.2 Best-BlastP=> >nrprot 48% Identities = 70/252 (27%), Positives = 135/252 (53%), Gaps = 4/252 (1%) ref|NP_784615.1| integral membrane protein [Lactobacillus plantarum WCFs1] emb|CAD63460.1| integral membrane protein [Lactobacillus plantarum WCFs1] Length = 293

44.1 Best-BlastP=> >nrprot 97% Identities = 335/346 (96%), Positives = 339/346 (97%) gb|AAM08244.1| probable conjugal transfer protein [Legionella pneumophila] Length = 346

440.4 Best-BlastP=> >nrprot 14% Identities = 134/534 (25%), Positives = 215/534 (40%), Gaps = 106/534 (19%) pir|JC6009 surface-located membrane protein Imp3 precursor - *Mycoplasma hominis* emb|CAA64858.1| Imp3 protein [Mycoplasma hominis] Length = 1302

4402.2 Best-BlastP=> >nrprot 65% Identities = 83/174 (47%), Positives = 119/174 (68%), Gaps = 2/174 (1%) ref|NP_930722.1| hypothetical protein [Photobacterium luminescens subsp. laumontii TTO1] Length = 176

4403.2 Best-BlastP=> >nrprot 60% Identities = 124/258 (48%), Positives = 160/258 (62%) ref|NP_252268.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9HY42|YZ78_PSEAE Hypothetical protein PA3578 pir|IE83199 conserved hypothetical protein PA3578 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AG06966.1|AE004778_10 conserved hypothetical protein [Pseudomonas aeruginosa PA01] Length = 261

4404.1 Best-BlastP=> >nrprot 49% Identities = 51/124 (41%), Positives = 69/124 (55%) ref|NP_105863.1| transcriptional regulator [Mesorhizobium loti] dbj|BAB51649.1| transcriptional regulator [Mesorhizobium loti] Length = 143

4405.1 Best-BlastP=> >nrprot 73% Identities = 77/148 (52%), Positives = 112/148 (75%) ref|NP_662760.1| conserved hypothetical protein [Chlorobium tepidum TLS] gb|AAM73102.1| conserved hypothetical protein [Chlorobium tepidum TLS] Length = 155

4406.1 Best-BlastP=> >nrprot 63% Identities = 78/187 (41%), Positives = 121/187 (64%), Gaps = 1/187 (0%) ref|ZP_00092584.1| COG1278: Cold shock proteins [Azotobacter vinelandii] Length = 333

4407.1 Best-BlastP=> >nrprot 65% Identities = 39/69 (56%), Positives = 51/69 (73%) ref|NP_743260.1| cold-shock domain family protein [Pseudomonas putida KT2440] gb|AAN66724.1|AE016300_9 cold-shock domain family protein [Pseudomonas putida KT2440] Length = 69

4408.1 Best-BlastP=> >nrprot No Hits found

4409.1 Best-BlastP=> >nrprot 71% Identities = 120/212 (56%), Positives = 150/212 (70%), Gaps = 3/212 (1%) ref|NP_403711.1| orotate phosphoribosyltransferase [Yersinia pestis] ref|NP_667439.1| orotate phosphoribosyltransferase [Yersinia pestis KIM] sp|Q8ZJP7|PYRE_YERPE Orotate phosphoribosyltransferase (OPRT) (OPRTase) pir|AF0006 orotate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Yersinia pestis (strain CC92) emb|CAC889191.1| orotate phosphoribosyltransferase [Yersinia pestis CO92] gb|AM83690.1|AE013610_2 orotate phosphoribosyltransferase [Yersinia pestis KIM] Length = 215

4415.3 Best-BlastP=> >nrprot 55% Identities = 157/417 (37%), Positives = 239/417 (57%), Gaps = 8/417 (1%) ref|ZP_00034486.1| COG0642: Signal transduction histidine kinase [Burkholderia fungorum] Length = 479

4419.2 Best-BlastP=> >nrprot 72% Identities = 161/317 (50%), Positives = 233/317 (73%) ref|NP_794895.1| proline iminopeptidase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58590.1| proline iminopeptidase [Pseudomonas syringae pv. tomato str. DC3000] Length = 323

4421.2 Best-BlastP=> >nrprot 41% Identities = 77/254 (30%), Positives = 111/254 (43%), Gaps = 51/254 (20%) ref|NP_052363.1| unnamed protein product [Coxiella burnetii] ref|NP_819024.1| hypothetical protein [Coxiella burnetii RSA 493] pir|S38245 hypothetical protein - Coxiella burnetii emb|CAA53133.1| unnamed protein product [Coxiella burnetii] gb|AAO91584.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 341

4422.1 Best-BlastP=> >nrprot No Hits found

4424.1 Best-BlastP=> >nrprot No Hits found

4425.1 Best-BlastP=> >nrprot 46% Identities = 57/160 (35%), Positives = 80/160 (50%), Gaps = 3/160 (1%) ref|NP_105070.1| hypothetical protein, acetyltransferase, putative [Mesorhizobium loti] dbj|BAB50856.1| hypothetical protein [Mesorhizobium loti] Length = 168

4427.1 Best-BlastP=>>nrprot No Hits found

4428.1 Best-BlastP=>>nrprot No Hits found

4429.2 Best-BlastP=>>nrprot No Hits found

443.3 Best-BlastP=>>nrprot 99% Identities = 190/191 (99%), Positives = 191/191 (100%) pir|[T18327 icmQ protein - Legionella pneumophila emb|CAA73239.1| lcmQ protein [Legionella pneumophila] Length = 191

4431.2 Best-BlastP=>>nrprot 14% Identities = 61/293 (20%), Positives = 128/293 (43%), Gaps = 33/293 (11%) dbj|BAC86266.1| unnamed protein product [Homo sapiens] Length = 486

4432.2 Best-BlastP=>>nrprot No Hits found

4433.1 Best-BlastP=>>nrprot 42% Identities = 64/200 (32%), Positives = 86/200 (43%), Gaps = 12/200 (6%) ref|NP_799850.1| putative tellurite resistance protein-related protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61683.1| putative tellurite resistance protein-related protein [Vibrio parahaemolyticus] Length = 195

4434.1 Best-BlastP=>>nrprot 34% Identities = 52/215 (24%), Positives = 91/215 (42%), Gaps = 23/215 (10%) ref|NP_788733.1| multiple ankyrin repeats single KH domain CG33106-PA [Drosophila melanogaster] ref|NP_788734.1| multiple ankyrin repeats single KH domain CG33106-PB [Drosophila melanogaster] gb|AAO41600.1| CG33106-PA [Drosophila melanogaster] gb|AAO41601.1| CG33106-PB [Drosophila melanogaster] Length = 4001

4435.4 Best-BlastP=>>nrprot 13% Identities = 50/196 (25%), Positives = 92/196 (46%), Gaps = 32/196 (16%) ref|NP_001804.1| centromere protein E; Centromere autoantigen E (312kD); centromere protein E (312kD); kinesin family member 10 [Homo sapiens] sp|Q02224|CENE_HUMAN Centromeric protein E (CENPE protein) pir|S28261 centromere protein E - human emb|CAA78727.1| CENPE

444.2 Best-BlastP=>>nrprot 96% Identities = 116/120 (96%), Positives = 117/120 (97%) pir|[T18326 icmR protein - Legionella pneumophila emb|CAA73238.1| lcmR protein [Legionella pneumophila] emb|CAA75323.1| lcmR protein [Legionella pneumophila] Length = 120

4440.1 Best-BlastP=>>nrprot 73% Identities = 71/144 (49%), Positives = 104/144 (72%), Gaps = 4/144 (2%) ref|ZP_00065054.1| COG1558: Flagellar basal body rod protein [Microbulbifer degradans] 2-40 Length = 148

4441.1 Best-BlastP=>>nrprot 61% Identities = 61/132 (46%), Positives = 80/132 (60%), Gaps = 1/132 (0%) gb|AN08637.1| FlgB [Aeromonas hydrophilia] Length = 132

4442.1 Best-BlastP=>>nrprot 75% Identities = 202/297 (68%), Positives = 235/297 (79%) ref|NP_928683.1| oxygen-dependent coproporphyrinogen III oxidase [Photorhabdus luminescens subsp. laumontii TTO1] Length = 302

4444.2 Best-BlastP=>>nrprot 57% Identities = 168/420 (40%), Positives = 249/420 (59%), Gaps = 12/420 (2%) ref|ZP_00030428.1| COG0477: Permeases of the major facilitator superfamily [Burkholderia fungorum] Length = 645

4452.2 Best-BlastP=>>nrprot 34% Identities = 127/238 (53%), Positives = 161/238 (67%) ref|ZP_00112372.1| COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Nostoc punctiforme] Length = 616

4453.2 Best-BlastP=>>nrprot 41% Identities = 97/469 (20%), Positives = 194/469 (41%), Gaps = 60/469 (12%) gb|EAA15516.1| hypothetical protein [Plasmidium yoelii yoelii] Length = 585

4454.4 Best-BlastP=>>nrprot 87% Identities = 258/329 (78%), Positives = 290/329 (88%) gb|AAB58447.1| spectinomycin phosphotransferase [Legionella pneumophila] Length = 331

4457.2 Best-BlastP=>>nrprot 51% Identities = 102/334 (30%), Positives = 174/334 (52%), Gaps = 14/334 (4%) ref|NP_249522.1| transcriptional regulator OruR [Pseudomonas aeruginosa PA01] ref|ZP_00138425.1| COG2207: AraC-type DNA-binding domain-containing proteins [Pseudomonas aeruginosa UCBPP-PA14] sp|P72171|OruR_PSEAE Ornithine utilization regulator pir|G83540 transcription regulator OruR PA0831 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AA894774.1| OruR [Pseudomonas aeruginosa] Length = 339
gb|AG04220.1|AE004518_1 transcriptional regulator OruR [Pseudomonas aeruginosa PAO1]

4462.3 Best-BlastP=>>nrprot 71% Identities = 115/192 (59%), Positives = 145/192 (75%) ref|ZP_00067991.1| COG0088: Ribosomal protein L4 [Microbulbifer degradans 2-40] Length = 204

4463.2 Best-BlastP=>>nrprot 80% Identities = 138/209 (66%), Positives = 175/209 (83%), Gaps = 1/209 (0%) ref|NP_403860.1| 50S ribosomal protein L3 [Yersinia pestis] ref|NP_671283.1| 50S ribosomal subunit protein L3 [Yersinia pestis KIM] pir|AB0026 50S ribosomal protein L3 [imported] - Yersinia pestis (strain CO92) emb|CAC89069.1| 50S ribosomal protein L3 [Yersinia pestis CO92] gb|AAM87534.1|AE014002_7 50S ribosomal subunit protein L3 [Yersinia pestis KIM] Length = 209

4464.1 Best-BlastP=>>nrprot 87% Identities = 86/103 (83%), Positives = 93/103 (90%) ref|NP_778069.1| 30S ribosomal protein S10 [Buchnera aphidicola (Baizongia pistaciae)] sp|Q89A67|RS10_BUCCBP 30S ribosomal protein S10 gb|AAO27174.1| 30S ribosomal protein S10 [Buchnera aphidicola str. Bp (Baizongia pistaciae)] Length = 104

4465.3 Best-BlastP=>>nrprot 37% Identities = 43/118 (36%), Positives = 61/118 (51%), Gaps = 10/118 (8%) pir|H71023 hypothetical protein PH1485 - Pyrococcus horikoshii dbj|BA30592.1| 156aa long hypothetical protein [Pyrococcus horikoshii] Length = 156

4466.3 Best-BlastP=>>nrprot 93% Identities = 338/397 (85%), Positives = 370/397 (93%), Gaps = 1/397 (0%) ref|ZP_00090901.1| COG0050: GTPases - translation elongation factors [Azotobacter vinelandii] Length = 397

4468.2 Best-BlastP=>>nrprot 89% Identities = 527/691 (76%), Positives = 621/691 (89%) ref|NP_819279.1| translation elongation factor G [Coxiella burnetii RSA 493] Length = 699

4469.2 Best-BlastP=>>nrprot 48% Identities = 86/277 (31%), Positives = 138/277 (49%), Gaps = 23/277 (8%) ref|NP_519890.1| PROBABLE OXIDOREDUCTASE DEHYDROGENASE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] emb|CAD15471.1| PROBABLE OXIDOREDUCTASE DEHYDROGENASE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] Length = 300

447.2 Best-BlastP=>>nrprot 99% Identities = 114/114 (100%), Positives = 114/114 (100%) pir|T18325 icmS protein - Legionella pneumophila emb|CAA73237.1| icmS protein [Legionella pneumophila] emb|CAA75322.1| icmS protein [Legionella pneumophila] Length = 114

4470.1 Best-BlastP=>>nrprot 64% Identities = 156/329 (47%), Positives = 223/329 (67%), Gaps = 6/329 (1%) ref|NP_742587.1| anthranilate phosphoribosyltransferase [Pseudomonas putida KT2440] sp|Q88Q77|TRPD_PSEPK Anthranilate phosphoribosyltransferase gb|AN66051.1|AE016234_4 anthranilate phosphoribosyltransferase [Pseudomonas putida KT2440] Length = 349

4471.3 Best-BlastP=>>nrprot 43% Identities = 47/160 (29%), Positives = 83/160 (51%), Gaps = 2/160 (1%) ref|NP_819774.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AA090288.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 195

4472.2 Best-BlastP=> >nprot 59% Identities = 116/247 (46%), Positives = 155/247 (62%), Gaps = 1/247 (0%) refNP_902024.1| probable hydrolase [Chromobacterium violaceum ATCC 12472] gb|AAQ60026.1| probable hydrolase [Chromobacterium violaceum ATCC 12472] Length = 267

4473.4 Best-BlastP=> >nprot 59% Identities = 89/180 (49%), Positives = 122/180 (67%), Gaps = 1/180 (0%) refZP_00092748.1| hypothetical protein [Azotobacter vinelandii] Length = 397

4474.1 Best-BlastP=> >nprot 52% Identities = 45/114 (39%), Positives = 65/114 (57%), Gaps = 4/114 (3%) refZP_00092749.1| hypothetical protein [Azotobacter vinelandii] Length = 135

4475.1 Best-BlastP=> >nprot 42% Identities = 51/183 (27%), Positives = 96/183 (52%), Gaps = 14/183 (7%) refZP_00047462.1| COG4123: Predicted O-methyltransferase [Lactobacillus gasseri] Length = 338

4477.2 Best-BlastP=> >nprot 46% Identities = 204/834 (24%), Positives = 357/834 (42%), Gaps = 142/834 (17%) refNP_907987.1| PHOSPHOENOLPYRUVATE CARBOXYLASE PEPCASE PEPC [Wolinella succinogenes] emb|CAE10887.1| PHOSPHOENOLPYRUVATE CARBOXYLASE PEPCASE PEPC [Wolinella succinogenes] Length = 885

4479.2 Best-BlastP=> >nprot 60% Identities = 46/119 (38%), Positives = 71/119 (59%), Gaps = 3/119 (2%) refNP_769098.1| blr2458 [Bradyrhizobium japonicum] dbj|BAC47723.1| blr2458 [Bradyrhizobium japonicum USDA 110] Length = 163

4480.1 Best-BlastP=> >nprot 98% Identities = 86/86 (100%), Positives = 86/86 (100%) pir|T18324 icmT protein - Legionella pneumophila emb|CAA73236.1| icmT protein [Legionella pneumophila] Length = 86

4480.4 Best-BlastP=> >nprot 69% Identities = 234/416 (56%), Positives = 291/416 (69%) refNP_812629.1| gamma-glutamyl phosphate reductase [Bacteroides thetaiotaomicron VPI-5482] gb|AAO78823.1| gamma-glutamyl phosphate reductase [Bacteroides thetaiotaomicron VPI-5482] Length = 417

4481.1 Best-BlastP=> >nprot 70% Identities = 91/172 (52%), Positives = 124/172 (72%), Gaps = 3/172 (1%) refNP_177142.1| expressed protein [Arabidopsis thaliana] ref|NP_849870.1| expressed protein [Arabidopsis thaliana] pir|F96720 unknown protein, 58197-59415 [imported] - Arabidopsis thaliana gb|AAG52556.1|AC010675_4 unknown protein; 58197-59415 [Arabidopsis thaliana] gb|AAM20691.1| unknown protein [Arabidopsis thaliana] gb|AAN15655.1| unknown protein [Arabidopsis thaliana] Length = 286

4482.1 Best-BlastP=> >nprot 56% Identities = 119/320 (37%), Positives = 168/320 (52%), Gaps = 33/320 (10%) refZP_00119712.1| COG4823: Abortive infection bacteriophage resistance protein [Cytophaga hutchinsonii] Length = 331

4483.2 Best-BlastP=> >nprot 98% Identities = 252/254 (99%), Positives = 252/254 (99%) gb|AAM73853.1|AF454864_1 putative lipase LipB [Legionella pneumophila] Length = 254

4484.1 Best-BlastP=> >nprot No Hits found

4485.2 Best-BlastP=> >nprot 98% Identities = 252/254 (99%), Positives = 252/254 (99%) gb|AAM73853.1|AF454864_1 putative lipase LipB [Legionella pneumophila] Length = 254

4487.1 Best-BlastP=> >nprot 70% Identities = 133/223 (59%), Positives = 163/223 (73%) refNP_231545.1| orotidine 5'-phosphate decarboxylase [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KQ77|PYRF_VIBCH Orotidine 5'-phosphate decarboxylase (OMP decarboxylase) (OMPDCase) (OMPdecase) pir|A82143 orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) VC1911 [similarity] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95059.1| orotidine 5'-phosphate decarboxylase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 231

4488.1 Best-BlastP=> >nrprot 72% Identities = 213/362 (58%), Positives = 270/362 (74%) ref|NP_903794.1| probable aminotransferase [Chromobacterium violaceum ATCC 12472] gb|AAQ61785.1| probable aminotransferase [Chromobacterium violaceum ATCC 12472] Length = 365

4489.3 Best-BlastP=> >nrprot 67% Identities = 195/383 (50%), Positives = 263/383 (68%), Gaps = 2/383 (0%) ref|NP_819562.1| TPR domain protein [Coxiella burnetii RSA 493] gb|AAO90076.1| TPR domain protein [Coxiella burnetii RSA 493] Length = 388

4490.2 Best-BlastP=> >nrprot 38% Identities = 65/177 (36%), Positives = 109/177 (61%), Gaps = 12/177 (6%) ref|NP_808996.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO75190.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Length = 288

4491.3 Best-BlastP=> >nrprot No Hits found

4492.3 Best-BlastP=> >nrprot No Hits found

4493.1 Best-BlastP=> >nrprot No Hits found

4496.2 Best-BlastP=> >nrprot 51% Identities = 106/240 (44%), Positives = 141/240 (58%), Gaps = 3/240 (1%) emb|CAB60048.1| lvrA [Legionella pneumophila] Length = 288

4497.4 Best-BlastP=> >nrprot No Hits found

4498.1 Best-BlastP=> >nrprot No Hits found

45.1 Best-BlastP=> >nrprot 94% Identities = 115/131 (87%), Positives = 125/131 (95%) gb|AAM08243.1| LvrD [Legionella pneumophila] Length = 131

4497.4 Best-BlastP=> >nrprot 39% Identities = 22/50 (44%), Positives = 28/50 (56%) gb|AAF87782.1|AF279293_1 p76 membrane protein precursor [Mycoplasma hypopneumoniae] Length = 1427

4500.1 Best-BlastP=> >nrprot 82% Identities = 69/116 (59%), Positives = 97/116 (83%) ref|ZP_00067079.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 117

4503.1 Best-BlastP=> >nrprot 77% Identities = 209/334 (62%), Positives = 266/334 (79%) ref|NP_744617.1| phenylalanyl-tRNA synthetase, alpha subunit [Pseudomonas putida KT2440] gb|AAN68081.1|AE016440_1 phenylalanyl-tRNA synthetase, alpha subunit [Pseudomonas putida KT2440] Length = 338

4505.3 Best-BlastP=> >nrprot 88% Identities = 98/118 (83%), Positives = 106/118 (89%) ref|NP_929901.1| 50S ribosomal protein L20 [Photorhabdus laumondii TTO1] Length = 118

4508.4 Best-BlastP=> >nrprot 77% Identities = 90/161 (55%), Positives = 126/161 (78%) ref|NP_719351.1| conserved hypothetical protein [Shewanella oneidensis MR-1] sp|Q8EAS7|Y2B5_SHEON Hypothetical UPF0234 protein SO3815 gb|AN56795.1|AE015815_1 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 161

451.3 Best-BlastP=> >nrprot No Hits found

4510.1 Best-BlastP=> >nrprot 83% Identities = 545/812 (67%), Positives = 672/812 (82%), Gaps = 10/812 (1%) ref|NP_819766.1| ATP-dependent protease La [Coxiella burnetii RSA 493] gb|AAO90280.1| ATP-dependent protease La [Coxiella burnetii RSA 493] Length = 817

4511.1 Best-BlastP=> >nrprot 70% Identities = 53/90 (58%), Positives = 66/90 (73%) ref|ZP_00119213.1| COG0776: Bacterial nucleoid DNA-binding protein [Cytophaga hutchinsonii] Length = 90

4512.4 Best-BlastP=>>nrprot 49% Identities = 181/604 (29%), Positives = 311/604 (51%), Gaps = 28/604 (4%) ref|ZP_00139461.1| COG0760: Parvulin-like peptidyl-prolyl isomerase [Pseudomonas aeruginosa UCBPP-PA14] Length = 621

4516.3 Best-BlastP=>>nrprot 56% Identities = 157/337 (46%), Positives = 214/337 (63%), Gaps = 3/337 (0%) ref|ZP_00030194.1| COG0845: Membrane-fusion protein [Burkholderia fungorum] Length = 513

4517.2 Best-BlastP=>>nrprot 51% Identities = 97/274 (35%), Positives = 145/274 (52%), Gaps = 21/274 (7%) gb|AAK81664.1| MdcB [Burkholderia cepacia] Length = 290

4519.3 Best-BlastP=>>nrprot 78% Identities = 341/546 (62%), Positives = 431/546 (78%), Gaps = 2/546 (0%) ref|NP_640913.1| alpha subunit of malonate decarboxylase [Xanthomonas axonopodis pv. citri str. 306] gb|AAM35449.1| alpha subunit of malonate decarboxylase [Xanthomonas axonopodis pv. citri str. 306] Length = 548

4520.1 Best-BlastP=>>nrprot 73% Identities = 225/396 (56%), Positives = 299/396 (75%), Gaps = 2/396 (0%) spi|Q8GDU2|ASSY_HELMO Argininosuccinate synthase (Citrulline--aspartate ligase) gb|AAN87486.1| Argininosuccinate synthase [Helicobacillus mobilis] Length = 408

4521.1 Best-BlastP=>>nrprot 60% Identities = 96/207 (46%), Positives = 135/207 (65%), Gaps = 15/207 (7%) ref|NP_465264.1| similar to amino acid (glutamine) ABC transporter (ATP-binding protein) [Listeria monocytogenes EGD-e] pir|AC1292 amino acid (glutamine) ABC transporter (ATP-binding protein) homolog lmo1739 [imported] - Listeria monocytogenes (strain EGD-e) emb|CAC99817.1| lmo1739 [Listeria monocytogenes] Length = 215

4522.4 Best-BlastP=>>nrprot 66% Identities = 94/203 (46%), Positives = 144/203 (70%), Gaps = 2/203 (0%) ref|NP_359808.1| amino acid ABC transporter permease protein [Rickettsia conorii] ref|ZP_00142355.1| amino acid ABC transporter permease protein [Rickettsia sibirica] pir|C97721 amino acid ABC transporter permease protein yqiY [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02709.1| amino acid ABC transporter permease protein [Rickettsia conorii] gb|EAA25764.1| amino acid ABC transporter permease protein [Rickettsia sibirica] Length = 218

4523.1 Best-BlastP=>>nrprot 49% Identities = 56/159 (35%), Positives = 89/159 (55%), Gaps = 4/159 (2%) ref|NP_714273.1| MutT/nudix family protein [Leptospira interrogans serovar lai str. 56601] gb|AAN51291.1|AE011563_7 MutT/nudix family protein [Leptospira interrogans serovar lai str. 56601] Length = 223

4524.1 Best-BlastP=>>nrprot 52% Identities = 79/246 (32%), Positives = 125/246 (50%), Gaps = 11/246 (4%) ref|NP_670144.1| arginine 3rd transport system periplasmic binding protein [Yersinia pestis KIM] gb|AAM86395.1|AE013887_2 arginine 3rd transport system periplasmic binding protein [Yersinia pestis KIM] Length = 252

4525.2 Best-BlastP=>>nrprot 73% Identities = 317/556 (57%), Positives = 418/556 (75%), Gaps = 2/556 (0%) ref|NP_718167.1| long-chain-fatty-acid-CoA ligase [Shewanella oneidensis MR-1] gb|AAN5561.1|AE015699_9 long-chain-fatty-acid-CoA ligase [Shewanella oneidensis MR-1] Length = 557

4526.3 Best-BlastP=>>nrprot 83% Identities = 64/111 (57%), Positives = 93/111 (83%), Gaps = 2/111 (1%) ref|ZP_00065090.1| COG1886: Flagellar motor switch/type III secretion pathway protein [Microbulifer degradans 2-40] Length = 141

4528.2 Best-BlastP=>>nrprot 21% Identities = 42/73 (57%), Positives = 56/73 (76%) gb|AN34372.1| ORF2 transposase [Acinetobacter baumannii] Length = 76

453.3 Best-BlastP=>>nrprot 87% Identities = 181/244 (74%), Positives = 220/244 (90%), Gaps = 6/244 (2%) ref|ZP_00023826.1| COG0330: Membrane protease subunits, stomatin/prohibitin homologs [Ralstonia metallidurans] Length = 251

4530.1 Best-BlastP=>>nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614_2 unknown [Francisella tularensis subsp. tularensis] Length = 94

4531.2 Best-BlastP=>>nrprot 53% Identities = 34/77 (44%), Positives = 47/77 (61%), Gaps = 5/77 (6%) gb|AAG53985.1|AF327444_1 putative transposase A [Pantoea agglomerans] Length = 149

4532.2 Best-BlastP=>>nrprot 30% Identities = 127/185 (68%), Positives = 148/185 (80%), Gaps = 11/185 (5%) emb|CAC33489.1| hypothetical protein [Legionella pneumophila] Length = 189

4533.2 Best-BlastP=>>nrprot 50% Identities = 643/2158 (29%), Positives = 955/2158 (44%), Gaps = 397/2158 (18%) ref|NP_758987.1| unknown [Zymomonas mobilis] gb|AAL36122.1| unknown [Zymomonas mobilis] Length = 2201

4535.2 Best-BlastP=>>nrprot 69% Identities = 226/438 (51%), Positives = 312/438 (71%), Gaps = 18/438 (4%) ref|ZP_00089764.1| COG0793: Periplasmic protease [Azotobacter vinelandii] Length = 456

4536.1 Best-BlastP=>>nrprot 49% Identities = 114/349 (32%), Positives = 189/349 (54%), Gaps = 12/349 (3%) ref|ZP_00065627.1| COG4942: Membrane-bound metallopeptidase [Microbulbifer degradans] 2-40] Length = 402

4538.2 Best-BlastP=>>nrprot 68% Identities = 273/506 (53%), Positives = 353/506 (69%), Gaps = 4/506 (0%) ref|ZP_00141602.1| COG0696: Phosphoglyceromutase [Pseudomonas aeruginosa UCBPP-PA14] Length = 515

454.1 Best-BlastP=>>nrprot 59% Identities = 215/454 (47%), Positives = 301/454 (66%), Gaps = 31/454 (6%) ref|NP_820466.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90980.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 458

4540.2 Best-BlastP=>>nrprot No Hits found

4542.4 Best-BlastP=>>nrprot 35% Identities = 136/313 (43%), Positives = 191/313 (61%), Gaps = 22/313 (7%) ref|ZP_00033133.1| COG2010: Cytochrome c, mono- and diheme variants [Burkholderia fungorum] Length = 432

4546.3 Best-BlastP=>>nrprot 21% Identities = 47/163 (28%), Positives = 74/163 (45%), Gaps = 18/163 (11%) ref|ZP_00011332.1| COG0183: Acetyl-CoA acetyltransferase [Rhodopseudomonas palustris] Length = 504

4547.4 Best-BlastP=>>nrprot 76% Identities = 206/337 (61%), Positives = 260/337 (77%), Gaps = 3/337 (0%) ref|ZP_00125317.1| COG0604: NADPH:quinone reductase and related Zn-dependent oxidoreductases [Pseudomonas syringae pv. syringae B728a] Length = 337

4549.2 Best-BlastP=>>nrprot 21% Identities = 73/109 (66%), Positives = 94/109 (86%) ref|NP_820449.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90963.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 113

4551.2 Best-BlastP=>>nrprot 55% Identities = 31/78 (39%), Positives = 49/78 (62%) ref|NP_875585.1| Uncharacterized conserved membrane protein [Prochlorococcus marinus subsp. marinus str. CCMP1375] gb|AAQ00238.1| Uncharacterized conserved membrane protein [Prochlorococcus marinus subsp. marinus str. CCMP1375] Length = 91

4552.4 Best-BlastP=>>nrprot No Hits found

4553.2 Best-BlastP=>>nrprot 66% Identities = 107/240 (44%), Positives = 156/240 (65%), Gaps = 14/240 (5%) ref|NP_867184.1| short chain alcohol dehydrogenase-like [Pirellula sp.] emb|CAD74729.1| short chain alcohol dehydrogenase-like [Pirellula sp.] Length = 247

4554.2 Best-BlastP=>>nrprot 35% Identities = 27/49 (55%), Positives = 31/49 (63%), Gaps = 1/49 (2%) ref|ZP_00031568.1| COG1051: ADP-ribose pyrophosphatase [Burkholderia fungorum] Length = 181

4558.1 Best-BlastP=>>nrprot 29% Identities = 43/182 (23%), Positives = 82/182 (45%), Gaps = 9/182 (4%) gb|AAK27486.1|AF343323_1 DNA gyrase B [Cycloclasticus sp. NOP-122A] gb|AAK27491.1|AF343328_1 DNA gyrase B [Cycloclasticus sp. N-221A] gb|AAK27492.1|AF343329_1 DNA gyrase B [Cycloclasticus sp. N-231B] gb|AAK27493.1|AF343330_1 DNA gyrase B [Cycloclasticus sp. P-211A2] Length = 362

4559.1 Best-BlastP=>>nrprot 59% Identities = 206/502 (41%), Positives = 308/502 (61%), Gaps = 6/502 (1%) ref|NP_819464.1| amino acid permease family protein [Coxiella burnetii RSA 493] gb|AO89978.1| amino acid permease family protein [Coxiella burnetii RSA 493] Length = 531

4560.2 Best-BlastP=>>nrprot 26% Identities = 49/217 (22%), Positives = 98/217 (45%), Gaps = 30/217 (13%) ref|NP_702678.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1248

4561.2 Best-BlastP=>>nrprot 48% Identities = 140/428 (32%), Positives = 222/428 (51%), Gaps = 3/428 (0%) ref|NP_6368850.1| outer membrane component of multidrug efflux pump [Xanthomonas campestris str. ATCC 33913] gb|AAM40774.1| outer membrane component of multidrug efflux pump [Xanthomonas campestris str. ATCC 33913] Length = 467

4564.2 Best-BlastP=>>nrprot 99% Identities = 198/200 (99%), Positives = 199/200 (99%) gb|AAM00391.1|CcmA [Legionella pneumophila] Length = 200

4566.1 Best-BlastP=>>nrprot 62% Identities = 93/192 (48%), Positives = 124/192 (64%), Gaps = 5/192 (2%) ref|ZP_00071947.1| COG0693: Putative intracellular protease/aminidase [Trichodesmium erythraeum IIMS101] Length = 191

4567.2 Best-BlastP=>>nrprot 10% Identities = 44/175 (25%), Positives = 69/175 (39%), Gaps = 36/175 (20%) gb|AAK20704.1|AF316641_10 WcIT [Streptococcus pneumoniae] Length = 242

457.2 Best-BlastP=>>nrprot 50% Identities = 180/528 (34%), Positives = 271/528 (51%), Gaps = 58/528 (10%) ref|NP_820680.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AO91194.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 518

4571.2 Best-BlastP=>>nrprot 34% Identities = 29/58 (50%), Positives = 38/58 (65%) ref|NP_819567.1| lipoprotein, putative [Coxiella burnetii RSA 493] gb|AO90081.1| lipoprotein, putative [Coxiella burnetii RSA 493] Length = 323

4572.2 Best-BlastP=>>nrprot 63% Identities = 175/348 (50%), Positives = 227/348 (65%), Gaps = 2/348 (0%) ref|ZP_00068140.1| COG1194: A/G-specific DNA glycosylase [Microbulbifer degradans 2-40] Length = 355

4573.4 Best-BlastP=>>nrprot 43% Identities = 123/542 (22%), Positives = 226/542 (41%), Gaps = 78/542 (14%) ref|NP_819951.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AO90465.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 502

4574.2 Best-BlastP=>>nrprot 44% Identities = 95/367 (25%), Positives = 164/367 (44%), Gaps = 55/367 (14%) ref|ZP_00089878.1| COG1562: Phytoene/squalene synthetase [Azotobacter vinelandii] Length = 377

4577.2 Best-BlastP=>>nrprot 48% Identities = 101/231 (43%), Positives = 135/231 (58%), Gaps = 19/231 (8%) ref|NP_819994.1| rare lipoprotein A family protein [Coxiella burnetii RSA 493] gb|AO90508.1| rare lipoprotein A family protein [Coxiella burnetii RSA 493] Length = 261

4578.1 Best-BlastP=>>nrprot 80% Identities = 224/390 (57%), Positives = 314/390 (80%), Gaps = 1/390 (0%) ref|NP_819495.1| sodium/hydrogen antiporter family protein [Coxiella burnetii RSA 493] Length = 389

458.3 Best-BlastP=>>nrprot 47% Identities = 93/334 (27%), Positives = 164/334 (49%), Gaps = 18/334 (5%) ref|NP_819588.1| DNA polymerase III, delta subunit [Coxiella burnetii RSA 493] gb|AAO90102.1| DNA polymerase III, delta subunit [Coxiella burnetii RSA 493] Length = 339

4580.1 Best-BlastP=>>nrprot 34% Identities = 41/110 (37%), Positives = 58/110 (52%), Gaps = 3/110 (2%) ref|NP_742951.1| inner membrane protein AmpE [Pseudomonas putida KT2440] Length = 276

4581.2 Best-BlastP=>>nrprot 29% Identities = 22/97 (22%), Positives = 39/97 (40%), Gaps = 1/97 (1%) ref|NP_820299.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90813.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 155

4584.3 Best-BlastP=>>nrprot No Hits found

4587.2 Best-BlastP=>>nrprot No Hits found

4588.2 Best-BlastP=>>nrprot No Hits found

4589.1 Best-BlastP=>>nrprot No Hits found

459.3 Best-BlastP=>>nrprot 56% Identities = 76/212 (35%), Positives = 119/212 (56%), Gaps = 2/212 (0%) ref|NP_406133.1| putative nicotinate-nucleotide adenyltransferase [Yersinia pestis] sp|Q8ZDG1|NADD_YERPE Probable nicotinate-nucleotide adenyltransferase (Deamido-NAD(+) pyrophosphorylase) (Deamido-NAD(+) diphosphorylase) (Nicotinate mononucleotide adenyltransferase) (NaMN adenyltransferase) pirl|AC0318 probable nicotinate-nucleotide adenyltransferase (EC 2.7.7.18) [Imported] - Yersinia pestis (strain CO92) CO92] Length = 220

4590.1 Best-BlastP=>>nrprot 56% Identities = 57/130 (43%), Positives = 77/130 (59%), Gaps = 6/130 (4%) ref|ZP_00086142.1| COG2764: Uncharacterized protein conserved in bacteria [Pseudomonas fluorescens PfO-1] Length = 137

4591.2 Best-BlastP=>>nrprot 71% Identities = 86/155 (55%), Positives = 113/155 (72%), Gaps = 4/155 (2%) ref|ZP_00109160.1| COG3865: Uncharacterized protein conserved in bacteria [Nostoc punctiforme] Length = 165

4597.1 Best-BlastP=>>nrprot No Hits found

4598.2 Best-BlastP=>>nrprot 71% Identities = 132/248 (53%), Positives = 176/248 (70%), Gaps = 5/248 (2%) ref|NP_902034.1| acetooacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ60036.1| acetooacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] Length = 246

4599.2 Best-BlastP=>>nrprot 78% Identities = 135/206 (65%), Positives = 169/206 (82%) ref|ZP_00024696.1| COG1484: DNA replication protein [Ralstonia metallidurans] Length = 268

46.1 Best-BlastP=>>nrprot 97% Identities = 220/236 (93%), Positives = 230/236 (97%) gb|AAM08241.1| putative TraC protein [Legionella pneumophila] Length = 236

460.2 Best-BlastP=>>nrprot 53% Identities = 59/158 (37%), Positives = 95/158 (60%) ref|NP_819911.1| colicin V production protein [Coxiella burnetii RSA 493] gb|AAO90425.1| colicin V production protein [Coxiella burnetii RSA 493] Length = 184

4600.2 Best-BlastP=> >nrprot 52% Identities = 83/238 (34%), Positives = 128/238 (53%), Gaps = 27/238 (11%) ref|NP_932037.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] Length = 255

4601.1 Best-BlastP=> >nrprot No Hits found

4602.3 Best-BlastP=> >nrprot 99% Identities = 300/302 (99%), Positives = 302/302 (100%) emb|CAC14311.1| putative transcriptional regulator [Legionella pneumophila] Length = 302

4604.3 Best-BlastP=> >nrprot 48% Identities = 48/182 (26%), Positives = 91/182 (50%), Gaps = 12/182 (6%) ref|NP_251679.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|F83271 hypothetical protein PA2989 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG06377.1|AE004724_6 hypothetical protein PA2989 [Pseudomonas aeruginosa PAO1] Length = 254

4607.2 Best-BlastP=> >nrprot 79% Identities = 265/421 (62%), Positives = 335/421 (79%) ref|ZP_00092427.1| hypothetical protein [Azotobacter vinelandii] Length = 838

4608.1 Best-BlastP=> >nrprot 33% Identities = 34/111 (30%), Positives = 60/111 (54%), Gaps = 3/111 (2%) ref|NP_700535.1| hypothetical protein [Plasmidum falciparum 3D7] gb|AAN35259.1|AE014830_3 hypothetical protein [Plasmidum falciparum 3D7] Length = 426

4609.2 Best-BlastP=> >nrprot No Hits found

4613.3 Best-BlastP=> >nrprot 48% Identities = 121/487 (24%), Positives = 240/487 (49%), Gaps = 29/487 (5%) ref|NP_753921.1| Hypothetical transporter ydgr [Escherichia coli CFT073] gb|AAN80486.1|AE016761_61 Hypothetical transporter ydgr [Escherichia coli CFT073] Length = 500

4615.3 Best-BlastP=> >nrprot No Hits found

4616.2 Best-BlastP=> >nrprot 48% Identities = 93/315 (29%), Positives = 150/315 (47%), Gaps = 35/315 (11%) ref|NP_820641.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91155.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 429

4618.1 Best-BlastP=> >nrprot 58% Identities = 110/250 (44%), Positives = 151/250 (60%), Gaps = 7/250 (2%) dbj|BAB72031.1| lipopolysaccharide biosynthesis glycosyltransferase [Photobacterium damselaes subsp. piscicida] Length = 255

462.2 Best-BlastP=> >nrprot 44% Identities = 71/278 (25%), Positives = 116/278 (41%), Gaps = 35/278 (12%) ref|NP_718631.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56075.1|AE015743_3 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 281

4620.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614_2 unknown [Francisella tularensis subsp. tularensis] Length = 94

4623.2 Best-BlastP=> >nrprot 52% Identities = 66/169 (39%), Positives = 93/169 (55%), Gaps = 5/169 (2%) ref|NP_814807.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] gb|AAO80877.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] Length = 168

4625.2 Best-BlastP=> >nrprot 68% Identities = 162/307 (52%), Positives = 215/307 (70%), Gaps = 1/307 (0%) ref|NP_761810.1| S-malonyltransferase [Vibrio vulnificus CMCP6] gb|AAO11337.1|AE016807_56 S-malonyltransferase [Vibrio vulnificus CMCP6] Length = 307

4626.1 Best-BlastP=> >nrprot 72% Identities = 172/314 (54%), Positives = 231/314 (73%), Gaps = 3/314 (0%) ref|NP_930069.1| 3-oxoacyl-[acyl carrier-protein] synthase III (beta-ketoacyl-ACP synthase III) (KAS III) [Photorhabdus luminescens subsp. embl|CAE15209.1| 3-oxoacyl-[acyl carrier-protein] synthase III (beta-ketoacyl-ACP synthase III) (KAS III) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 317

4627.2 Best-BlastP=> >nrprot 72% Identities = 183/330 (55%), Positives = 241/330 (73%), Gaps = 2/330 (0%) ref|NP_819526.1| fatty acid/phospholipid synthesis protein PIsX [Coxiella burnetii RSA 493] sp|Q83E40|PLSX_COXBU Fatty acid/phospholipid synthesis protein pIsX gb|AAO90040.1| fatty acid/phospholipid synthesis protein PIsX [Coxiella burnetii RSA 493] Length = 343

4628.2 Best-BlastP=> >nrprot 78% Identities = 45/55 (81%), Positives = 50/55 (90%) ref|ZP_00135404.1| COG0333: Ribosomal protein L32 [Actinobacillus pleuropneumoniae serovar 1 str. 4074] ref|NP_873288.1| 50S ribosomal protein L32 [Haemophilus ducreyi 35000HP] gb|AAP95677.1| 50S ribosomal protein L32 [Haemophilus ducreyi 35000HP] Length = 56

4629.2 Best-BlastP=> >nrprot 33% Identities = 23/98 (23%), Positives = 48/98 (48%), Gaps = 1/98 (1%) ref|ZP_00136314.1| COG1399: Predicted metal-binding, possibly nucleic acid-binding protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 148

463.2 Best-BlastP=> >nrprot No Hits found

4632.1 Best-BlastP=> >nrprot No Hits found

4633.2 Best-BlastP=> >nrprot 82% Identities = 121/184 (65%), Positives = 154/184 (83%) ref|NP_842482.1| Uncharacterized protein family UPF0016 [Nitrosomonas europaea ATCC 19718] embl|CAD86405.1| Uncharacterized protein family UPF0016 [Nitrosomonas europaea ATCC 19718] Length = 192

4634.2 Best-BlastP=> >nrprot 52% Identities = 222/716 (31%), Positives = 348/716 (48%), Gaps = 80/716 (11%) ref|NP_924649.1| probable peptidase [Gloebacter violaceus] dbj|BAC89644.1| gll1703 [Gloebacter violaceus] Length = 730

4636.4 Best-BlastP=> >nrprot 4% Identities = 49/164 (29%), Positives = 74/164 (45%), Gaps = 12/164 (7%) ref|ZP_00009072.1| hypothetical protein [Rhodopseudomonas palustris] Length = 275

464.2 Best-BlastP=> >nrprot 60% Identities = 167/405 (41%), Positives = 258/405 (63%), Gaps = 4/405 (0%) ref|NP_819909.1| FolC bifunctional protein [Coxiella burnetii RSA 493] gb|AAO90423.1| FolC bifunctional protein [Coxiella burnetii RSA 493] Length = 416

4640.2 Best-BlastP=> >nrprot 74% Identities = 466/845 (55%), Positives = 627/845 (74%), Gaps = 12/845 (1%) ref|NP_820057.1| DNA mismatch repair protein MutS [Coxiella burnetii RSA 493] gb|AAO90571.1| DNA mismatch repair protein MutS [Coxiella burnetii RSA 493] Length = 859

4642.1 Best-BlastP=> >nrprot 63% Identities = 79/154 (51%), Positives = 107/154 (69%), Gaps = 1/154 (0%) ref|ZP_00025457.1| COG1546: Uncharacterized protein (competence- and mitomycin-induced) [Ralstonia metallidurans] Length = 200

4643.2 Best-BlastP=> >nrprot 56% Identities = 176/176 (100%), Positives = 176/176 (100%) emb|CAC33483.1| hypothetical protein [Legionella pneumophila] Length = 176

4644.3 Best-BlastP=> >nrprot 41% Identities = 95/419 (22%), Positives = 174/419 (41%), Gaps = 31/419 (7%) ref|ZP_00071833.1| hypothetical protein [Trichodesmium erythraeum IMS101] Length = 424

4645.2 Best-BlastP=> >nrprot 44% Identities = 96/328 (29%), Positives = 162/328 (49%), Gaps = 10/328 (3%) ref|ZP_00056223.1| COG0477: Permeases of the major facilitator superfamily [Magnetospirillum magnetotacticum] Length = 407

4647.2 Best-BlastP=> >nrprot 25% Identities = 54/234 (23%), Positives = 94/234 (40%), Gaps = 8/234 (3%) ref|ZP_00034418.1| COG0683: ABC-type branched-chain amino acid transport systems, periplasmic component [Burkholderia fungorum] Length = 451

4649.1 Best-BlastP=> >nrprot No Hits found

465.2 Best-BlastP=> >nrprot 75% Identities = 186/283 (65%), Positives = 222/283 (78%), Gaps = 3/283 (1%) ref|NP_819908.1| acetyl-CoA carboxylase, carboxyl transferase, beta subunit [Coxiella burnetii RSA 493] gb|AAO90422.1| acetyl-CoA carboxylase, carboxyl transferase, beta subunit [Coxiella burnetii RSA 493] Length = 291

4650.3 Best-BlastP=> >nrprot 45% Identities = 301/1302 (23%), Positives = 574/1302 (44%), Gaps = 91/1302 (6%) ref|NP_901766.1| probable transmembrane protein [Chromobacterium violaceum ATCC 12472] gb|AAQ59768.1| probable transmembrane protein [Chromobacterium violaceum ATCC 12472] Length = 1272

4652.2 Best-BlastP=> >nrprot 62% Identities = 51/115 (44%), Positives = 79/115 (68%) ref|NP_353968.1| AGR_C_1731p [Agrobacterium tumefaciens] pir|[H97474 hypothetical 14.1K protein in rpli-cpdb intergenic region [imported] - Agrobacterium tumefaciens (strain C58, Cereon)] gb|AAK86753.1| AGR_C_1731p [Agrobacterium tumefaciens str. C58 (Cereon)] Length = 190

4653.2 Best-BlastP=> >nrprot 26% Identities = 50/154 (32%), Positives = 79/154 (51%), Gaps = 17/154 (11%) ref|NP_440166.1| hypothetical protein [Synechocystis sp. PCC 6803] sp|P72831|YC98_SYNY3 Hypothetical protein slr1298 pir|[S74695 hypothetical protein slr1298 - Synechocystis sp. (strain PCC 6803) dbj|BA16846.1| ORF_ID|slr1298~hypothetical protein [Synechocystis sp. PCC 6803] Length = 755

4655.3 Best-BlastP=> >nrprot 47% Identities = 130/460 (28%), Positives = 216/460 (46%), Gaps = 31/460 (6%) ref|NP_840264.1| Outer membrane efflux protein [Nitrosomonas europaea ATCC 19718] emb|CAD84081.1| Outer membrane efflux protein [Nitrosomonas europaea ATCC 19718] Length = 516

4656.2 Best-BlastP=> >nrprot 26% Identities = 69/366 (18%), Positives = 161/366 (43%), Gaps = 26/366 (7%) ref|XP_2300851.2| similar to hypothetical protein [Rattus norvegicus] Length = 396

4657.1 Best-BlastP=> >nrprot 62% Identities = 94/202 (46%), Positives = 131/202 (64%), Gaps = 7/202 (3%) ref|NP_520142.1| PUTATIVE GST-RELATED PROTEIN [Ralstonia solanacearum] emb|CAD15723.1| PUTATIVE GST-RELATED PROTEIN [Ralstonia solanacearum] Length = 230

4658.2 Best-BlastP=> >nrprot 75% Identities = 94/134 (70%), Positives = 105/134 (78%), Gaps = 1/134 (0%) ref|NP_105189.1| organic hydroperoxide resistance protein [Mesorhizobium loti] dbj|BAB50975.1| organic hydroperoxide resistance protein [Mesorhizobium loti] Length = 137

4659.2 Best-BlastP=> >nrprot No Hits found

4660.2 Best-BlastP=> >nrprot No Hits found

4662.1 Best-BlastP=> >nrprot No Hits found

4663.3 Best-BlastP=> >nrprot 98% Identities = 288/297 (96%), Positives = 294/297 (98%) pir||A42596 major outer membrane protein - Legionella pneumophila gb|AAA25300.1| major outer membrane protein Length = 297

4665.2 Best-BlastP=> >nrprot 45% Identities = 244/604 (40%), Positives = 363/604 (60%), Gaps = 38/604 (6%) ref|NP_715981.1| sensory box protein [Shewanella oneidensis MR-1] gb|AAN53426.1|AE015481_9 sensory box protein [Shewanella oneidensis MR-1] Length = 1515

4666.2 Best-BlastP=> >nrprot 53% Identities = 118/339 (34%), Positives = 174/339 (51%), Gaps = 44/339 (12%) ref|NP_720115.1| ribonuclease, T2 family [Shewanella oneidensis MR-1] gb|AAN57559.1|AE015891_10 ribonuclease, T2 family [Shewanella oneidensis MR-1] Length = 384

4668.1 Best-BlastP=> >nrprot 25% Identities = 75/198 (37%), Positives = 112/198 (56%), Gaps = 1/198 (0%) ref|ZP_00054876.1| hypothetical protein [Magnetospirillum magnetotacticum] Length = 626

4669.2 Best-BlastP=> >nrprot 76% Identities = 487/1 (67%), Positives = 55/1 (77%), Gaps = 1/71 (1%) ref|NP_232566.1| cold shock transcriptional regulator CspA [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KN00|CSPA_VIBCH Cold shock-like protein cspA pir||G82492 cold shock transcription regulator CspA VCA0166 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF96079.1| cold shock transcriptional regulator CspA [Vibrio cholerae O1 biovar eltor str. N16961] Length = 70

4671.3 Best-BlastP=> >nrprot 58% Identities = 131/353 (37%), Positives = 208/353 (58%), Gaps = 5/353 (1%) ref|NP_243998.1| endo-1,4-beta-glucanase [Bacillus halodurans] pir||D84041 endo-1,4-beta-glucanase BH3132 [Imported] - Bacillus halodurans (strain C-125) dbj|AB06851.1| endo-1,4-beta-glucanase [Bacillus halodurans] Length = 361

4672.1 Best-BlastP=> >nrprot 67% Identities = 119/224 (53%), Positives = 161/224 (71%), Gaps = 2/224 (0%) ref|ZP_00131766.1| COG0220; Predicted S-adenosylmethionine-dependent methyltransferase [Haemophilus somnis 2336] Length = 251

4673.1 Best-BlastP=> >nrprot 83% Identities = 59/78 (75%), Positives = 66/78 (84%) ref|NP_439112.1| ribosomal protein L28 [Haemophilus influenzae Rd] sp|P44364|RL28_HAEIN 50S ribosomal protein L28 pir||E64104 ribosomal protein L28 - Haemophilus influenzae (strain Rd KW20) gb|AAC22612.1| ribosomal protein L28 (rl28) [Haemophilus influenzae Rd] Length = 78

4676.2 Best-BlastP=> >nrprot 73% Identities = 262/488 (53%), Positives = 342/488 (70%), Gaps = 32/488 (6%) dbj|BAC93212.1| DNA-directed RNA polymerase specialized sigma subunit [Vibrio vulnificus YJ016] Length = 487

4678.3 Best-BlastP=> >nrprot No Hits found

468.3 Best-BlastP=> >nrprot 76% Identities = 81/121 (66%), Positives = 99/121 (81%) ref|ZP_00089152.1| COG0251: Putative translation initiation inhibitor, ygfF family [Azotobacter vinelandii] Length = 234

4680.2 Best-BlastP=> >nrprot 74% Identities = 129/219 (58%), Positives = 169/219 (77%) ref|NP_642403.1| ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM36939.1| ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306] Length = 227

4683.3 Best-BlastP=> >nrprot 73% Identities = 215/417 (51%), Positives = 305/417 (73%), Gaps = 5/417 (1%) ref|NP_820008.1| lipoprotein ABC transporter, permease protein, putative [Coxiella burnetii RSA 493] Length = 414

4688.2 Best-BlastP=> >nrprot 73% Identities = 199/352 (56%), Positives = 275/352 (78%) ref|NP_643914.1| type II secretion system protein-like protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM38450.1| type II secretion system protein-like protein [Xanthomonas axonopodis pv. citri str. 306] Length = 377

469.3 Best-BlastP=> >nrprot 74% Identities = 411/703 (58%), Positives = 530/703 (75%), Gaps = 5/703 (0%) ref|NP_819346.1| guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase [Coxiella burnetii RSA 493] gb|AAO89860.1| guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase [Coxiella burnetii RSA 493] Length = 707

4690.2 Best-BlastP=> >nrprot 4% Identities = 21/50 (42%), Positives = 31/50 (62%) ref|NP_055206.1| cardiac ankyrin repeat protein; cytokine inducible nuclear protein [Homo sapiens] pir|A57291 cytokine inducible nuclear protein C193 - human emb|CAA58676.1| nuclear protein [Homo sapiens] Length = 319

4691.2 Best-BlastP=> >nrprot 82% Identities = 279/413 (67%), Positives = 356/413 (86%), Gaps = 3/413 (0%) ref|NP_670162.1| probable serine transporter [Yersinia pestis KIM] gb|AAM86413.1|AE013888_9 probable serine transporter [Yersinia pestis KIM] Length = 440

4692.5 Best-BlastP=> >nrprot 71% Identities = 232/427 (54%), Positives = 316/427 (74%), Gaps = 3/427 (0%) ref|NP_820015.1| adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Coxiella burnetii RSA 493] gb|AAO90529.1| adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Coxiella burnetii RSA 493] Length = 442

4694.1 Best-BlastP=> >nrprot 59% Identities = 187/507 (36%), Positives = 297/507 (58%), Gaps = 30/507 (5%) ref|NP_616892.1| serine-type D-Ala-D-Ala carboxypeptidase [Methanoscincus acetivorans str. C2A] gb|AAM05372.1| serine-type D-Ala-D-Ala carboxypeptidase [Methanoscincus acetivorans str. C2A] Length = 568

4695.1 Best-BlastP=> >nrprot No Hits found

4696.3 Best-BlastP=> >nrprot 31% Identities = 102/309 (33%), Positives = 170/309 (55%), Gaps = 8/309 (2%) ref|NP_461159.1| putative membrane protein involved in resistance to lambda and N4 phages [Salmonella typhimurium LT2] gb|AAL21118.1| putative membrane protein involved in resistance to lambda and N4 phages [Salmonella typhimurium LT2] Length = 518

4699.3 Best-BlastP=> >nrprot 85% Identities = 315/417 (75%), Positives = 364/417 (87%), Gaps = 5/417 (1%) ref|NP_793499.1| ATP-dependent Clp protease, ATP-binding subunit ClpX [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57194.1| ATP-dependent Clp protease, ATP-binding subunit ClpX [Pseudomonas syringae pv. tomato str. DC3000] Length = 427

47.1 Best-BlastP=> >nrprot 97% Identities = 784/826 (94%), Positives = 806/826 (97%) gb|AAM08240.1| putative type IV secretion protein B4 [Legionella pneumophila] Length = 826

470.3 Best-BlastP=> >nrprot 88% Identities = 48/68 (70%), Positives = 60/68 (88%) ref|ZP_00085276.1| COG1758: DNA-directed RNA polymerase, subunit K/omega [Pseudomonas fluorescens PfO-1] Length = 87

4701.2 Best-BlastP=> >nrprot 58% Identities = 118/269 (43%), Positives = 163/269 (60%), Gaps = 14/269 (5%) ref|NP_819610.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90124.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 273

4702.1 Best-BlastP=> >nrprot 65% Identities = 96/188 (51%), Positives = 131/188 (69%) ref|NP_819608.1| glycosyl transferase, group 2 family protein [Coxiella burnetii RSA 493] gb|AAO90122.1| glycosyl transferase, group 2 family protein [Coxiella burnetii RSA 493] Length = 324

4703.2 Best-BlastP=> >nrprot 48% Identities = 53/118 (44%), Positives = 79/118 (66%) ref|NP_900830.1| probable glycosyl transferase [Chromobacterium violaceum ATCC 12472] gb|AAQ58835.1| probable glycosyl transferase [Chromobacterium violaceum ATCC 12472] Length = 335

4704.2 Best-BlastP=> >nrprot 56% Identities = 81/220 (36%), Positives = 127/220 (57%), Gaps = 3/220 (1%) ref|ZP_00021591.1| COG3376: High-affinity nickel permease [Ralstonia metallidurans] Length = 278

4705.3 Best-BlastP=>>nrprot 31% Identities = 55/205 (26%), Positives = 94/205 (45%), Gaps = 29/205 (14%) ref|NP_052786.1| pXO1-90 [Bacillus anthracis] ref|NP_652888.1| S-layer protein, (pXO1-90) [Bacillus anthracis str. A2012] pir|B59102 hypothetical protein pXO1-90 - Bacillus anthracis virulence plasmid pXO1 gb|AAD32394.1| pXO1-90 [Bacillus anthracis str. A2012] Length = 652

4706.3 Best-BlastP=>>nrprot 86% Identities = 106/141 (75%), Positives = 123/141 (87%) dbj|BAC55152.1| nucleoside diphosphate kinase [Halomonas sp. #593] Length = 141

4709.1 Best-BlastP=>>nrprot 73% Identities = 213/358 (59%), Positives = 281/358 (78%), Gaps = 1/358 (0%) ref|NP_274327.1| conserved hypothetical protein [Neisseria meningitidis MC58] pir|B81098 conserved hypothetical protein NMB1308 [imported] - *Neisseria meningitidis* (strain MC58 serogroup B) gb|AAF41683.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 364

4710.1 Best-BlastP=>>nrprot 40% Identities = 70/205 (34%), Positives = 107/205 (52%) ref|NP_231252.1| fimbrial biogenesis and twitching motility protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir|F82178 probable fimbrial biogenesis and twitching motility protein VC1612 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94766.1| fimbrial biogenesis and twitching motility protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] Length = 237

4711.1 Best-BlastP=>>nrprot 41% Identities = 42/159 (26%), Positives = 78/159 (49%), Gaps = 21/159 (13%) ref|NP_820244.1| DNA-binding protein putative [Coxiella burnetii RSA 493] gb|AAO90758.1| DNA-binding protein, putative [Coxiella burnetii RSA 493] Length = 203

4712.2 Best-BlastP=>>nrprot 71% Identities = 250/418 (59%), Positives = 306/418 (73%), Gaps = 2/418 (0%) ref|ZP_00091666.1| COG0124: Histidyl-tRNA synthetase [Azotobacter vinelandii] Length = 428

4713.1 Best-BlastP=>>nrprot No Hits found

4714.1 Best-BlastP=>>nrprot 47% Identities = 102/310 (32%), Positives = 159/310 (51%), Gaps = 5/310 (1%) ref|NP_800300.1| putative Yhfp protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62133.1| putative Yhfp protein [Vibrio parahaemolyticus] Length = 334

4715.3 Best-BlastP=>>nrprot 48% Identities = 43/158 (27%), Positives = 80/158 (50%), Gaps = 7/158 (4%) ref|ZP_00084605.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 171

4716.2 Best-BlastP=>>nrprot 48% Identities = 88/323 (27%), Positives = 162/323 (50%), Gaps = 34/323 (10%) ref|ZP_00144869.1| Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb|IAA23536.1| Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 351

4718.1 Best-BlastP=>>nrprot No Hits found

4719.2 Best-BlastP=>>nrprot 42% Identities = 149/405 (36%), Positives = 217/405 (53%), Gaps = 35/405 (8%) pir|T03487 potential multicopper oxidase - Rhodobacter capsulatus gb|AAC16140.1| potential multicopper oxidase [Rhodobacter capsulatus] Length = 491

4721.1 Best-BlastP=>>nrprot 73% Identities = 107/205 (52%), Positives = 155/205 (75%) ref|NP_819344.1| guanylate kinase [Coxiella burnetii RSA 493] gb|AAO89858.1| guanylate kinase [Coxiella burnetii RSA 493] Length = 206

4721.2 Best-BlastP=>>nrprot 70% Identities = 91/161 (56%), Positives = 125/161 (77%), Gaps = 1/161 (0%) ref|NP_440113.1| spore maturation protein A [Synechocystis sp. PCC 6803] pir|S74646 spore maturation protein A - Synechocystis sp. (strain PCC 6803) dbj|BAA16798.1| spore maturation protein A [Synechocystis sp. PCC 6803] Length = 182

4724.2 Best-BlastP=>>nrprot 70% Identities = 98/199 (49%), Positives = 142/199 (71%), Gaps = 5/199 (2%) ref|NP_440119.1| spore maturation protein B [Synechocystis sp. PCC 6803] pir|[S74647 spore maturation protein B - Synechocystis sp. (strain PCC 6803) dbj|BAA16799.1| spore maturation protein B [Synechocystis sp. PCC 6803] Length = 217

4725.2 Best-BlastP=>>nrprot 31% Identities = 73/267 (27%), Positives = 111/267 (41%), Gaps = 62/267 (23%) ref|NP_230974.1| hypothetical protein VC1330 [Vibrio cholerae O1 biovar eltor str. N16961] pir|[B82212 hypothetical protein VC1330 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94488.1| hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 275

4726.1 Best-BlastP=>>nrprot No Hits found

4727.1 Best-BlastP=>>nrprot 42% Identities = 43/76 (56%), Positives = 57/76 (75%) ref|ZP_00101887.1| COG5394: Uncharacterized protein conserved in bacteria [Desulfobacterium hatfieldense] Length = 107

4729.3 Best-BlastP=>>nrprot 64% Identities = 111/246 (45%), Positives = 161/246 (65%), Gaps = 1/246 (0%) ref|NP_902034.1| acetooacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ60036.1| acetooacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] Length = 246

473.2 Best-BlastP=>>nrprot 63% Identities = 122/288 (42%), Positives = 183/288 (63%) ref|NP_229866.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|[C82350 conserved hypothetical protein VC0209 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93385.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 288

4732.3 Best-BlastP=>>nrprot 33% Identities = 30/96 (31%), Positives = 42/96 (43%), Gaps = 17/96 (17%) dbj|BAA89216.1| soluble cytochrome cA [Shewanella violacea] Length = 85

4733.2 Best-BlastP=>>nrprot 71% Identities = 154/296 (52%), Positives = 210/296 (70%), Gaps = 8/296 (2%) ref|NP_820374.1| translation elongation factor Ts [Coxiella burnetii] RSA 493] sp|[Q9X5U9|EFTS_COXBU Elongation factor Ts (EF-Ts) gb|AAD33343.1|AF127534_2 elongation factor Ts [Coxiella burnetii] gb|AAO90888.1| translation elongation factor Ts [Coxiella burnetii] RSA 493] Length = 296

4734.2 Best-BlastP=>>nrprot 65% Identities = 134/341 (39%), Positives = 213/341 (62%), Gaps = 16/341 (4%) ref|NP_439856.1| hypothetical protein [Haemophilus influenzae Rd] sp|[P45339|YJEQ_HAEIN Hypothetical protein H11714 pir|[B64176 hypothetical protein H11714 - Haemophilus influenzae (strain Rd KW20) gb|AAC23359.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 346

4736.2 Best-BlastP=>>nrprot 70% Identities = 219/403 (54%), Positives = 289/403 (71%), Gaps = 2/403 (0%) ref|NP_232075.1| tRNA nucleotidyltransferase [Vibrio cholerae O1 biovar eltor str. N16961] pir|[D82076 tRNA nucleotidyltransferase VC2446 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95588.1| tRNA nucleotidyltransferase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 403

4737.1 Best-BlastP=>>nrprot 79% Identities = 122/178 (68%), Positives = 149/178 (83%) ref|ZP_00066572.1| COG1949: Oligoribonuclease (3'-5' exoribonuclease) [Microbubifer degradans 2-40] Length = 185

4739.1 Best-BlastP=>>nrprot 81% Identities = 156/208 (75%), Positives = 180/208 (86%) ref|NP_841903.1| DUF208 [Nitrosomonas europaea ATCC 19718] emb|CAD85792.1| DUF208 [Nitrosomonas europaea ATCC 19718] Length = 215

474.2

Best-BlastP=> >nrprot 44% Identities = 24/107 (22%), Positives = 49/107 (45%) ref|NP_878011.1| Tn1546 transposase [Staphylococcus aureus] sp|Q06238|TNP6_ENTFC Transposase for transposon Tn1546 pir||A40628 probable transposase - Enterococcus faecium transposon Tn1546 gb|AA65951.1| transposase [Enterococcus faecium] gb|AAQ17155.1| Tn1546 transposase [Staphylococcus aureus] Length = 988

4740.2 Best-BlastP=> >nrprot 62% Identities = 137/287 (47%), Positives = 193/287 (67%), Gaps = 1/287 (0%) ref|NP_478257.1| cation efflux system protein [Nostoc sp. PCC 7120] pir||AG2540 cation efflux system protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120beta dbj|BAB77253.1| cation efflux system protein [Nostoc sp. PCC 7120] Length = 304

4742.3 Best-BlastP=> >nrprot 48% Identities = 85/305 (27%), Positives = 148/305 (48%), Gaps = 14/305 (4%) ref|NP_759924.1| Transcriptional regulator [Vibrio vulnificus CMCP6] gb|AAO09451.1|AE016800_56 Transcriptional regulator [Vibrio vulnificus CMCP6] dbj|BAC95964.1| transcriptional regulator [Vibrio vulnificus YJ016] Length = 313

4744.3 Best-BlastP=> >nrprot 40% Identities = 66/257 (25%), Positives = 119/257 (46%), Gaps = 35/257 (13%) ref|ZP_00143092.1| hypothetical protein [Rickettsia sibirica] gb|EA26501.1| unknown [Rickettsia sibirica] Length = 290

4746.1 Best-BlastP=> >nrprot 52% Identities = 34/80 (42%), Positives = 48/80 (60%), Gaps = 3/80 (3%) ref|NP_799393.1| putative signal peptide protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61277.1| putative signal peptide protein [Vibrio parahaemolyticus] Length = 86

4748.1 Best-BlastP=> >nrprot 71% Identities = 145/246 (58%), Positives = 182/246 (73%), Gaps = 2/246 (0%) ref|ZP_00028198.1| COG4689: Acetoacetate decarboxylase [Burkholderia fungorum] Length = 442

4749.2 Best-BlastP=> >nrprot 39% Identities = 206/416 (49%), Positives = 284/416 (68%), Gaps = 3/416 (0%) ref|NP_386185.1| PUTATIVE NADH DEHYDROGENASE TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] emb|CAC46658.1|PUTATIVE NADH DEHYDROGENASE TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] Length = 422

475.1 Best-BlastP=> >nrprot No Hits found

4751.2 Best-BlastP=> >nrprot 44% Identities = 161/483 (33%), Positives = 245/483 (50%), Gaps = 72/483 (14%) gb|AAN78225.1| class 4 metalloprotease [Chromobacterium violaceum] Length = 489

4752.2 Best-BlastP=> >nrprot 60% Identities = 120/275 (43%), Positives = 180/275 (65%) ref|ZP_00029901.1| COG0697: Permeases of the drug/metabolite transporter (DMT) superfamily [Burkholderia fungorum] Length = 341

4754.1 Best-BlastP=> >nrprot No Hits found

4755.2 Best-BlastP=> >nrprot 58% Identities = 74/170 (43%), Positives = 109/170 (64%) ref|NP_310486.1| hypothetical protein [Escherichia coli O157:H7] pir||C90936 hypothetical protein ECs2459 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) dbj|BAB35882.1| hypothetical protein [Escherichia coli O157:H7] Length = 182

4757.2 Best-BlastP=> >nrprot 53% Identities = 60/192 (31%), Positives = 105/192 (54%), Gaps = 3/192 (1%) ref|ZP_00111879.1| COG0259: Pyridoxamine-phosphate oxidase [Nostoc punctiforme] Length = 214

4758.2 Best-BlastP=> >nrprot 51% Identities = 44/92 (47%), Positives = 66/92 (71%) ref|NP_926536.1| unknown protein [Gloeobacter violaceus] dbj|BAC91531.1| gsi3590 [Gloeobacter violaceus] Length = 98

4759.2 Best-BlastP=> >nrprot 70% Identities = 142/258 (55%), Positives = 181/258 (70%), Gaps = 5/258 (1%) ref|NP_863091.1| putative oxidoreductase [Pseudomonas putida] gb|AAO64293.1| putative oxidoreductase [Pseudomonas putida] gb|AAP44207.1| putative dehydrogenase [Pseudomonas sp. ND6] Length = 257

4760.2 Best-BlastP=> >nrprot No Hits found

4763.2 Best-BlastP=> >nrprot 52% Identities = 133/408 (32%), Positives = 219/408 (53%), Gaps = 23/408 (5%) ref|NP_903521.1| probable prophage integrase [Chromobacterium violaceum ATCC 12472] gb|AAQ61513.1| probable prophage integrase [Chromobacterium violaceum ATCC 12472]
Length = 423

4764.2 Best-BlastP=> >nrprot No Hits found

4766.2 Best-BlastP=> >nrprot 74% Identities = 80/144 (55%), Positives = 108/144 (75%), Gaps = 1/144 (0%) ref|NP_820296.1| conserved hypothetical protein [Coxiella burnetii RSA 493] 9b|AAO90810.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 146

4767.2 Best-BlastP=> >nrprot 62% Identities = 36/93 (38%), Positives = 57/93 (61%), Gaps = 3/93 (3%) ref|NP_273838.1| conserved hypothetical protein [Neisseria meningitidis MC58] ref|NP_283783.1| hypothetical protein NMA1005 [Neisseria meningitidis 22491] sp|Q9JRC2|YA05_NEIMA Hypothetical protein NMA1005/NMB0796_prl|C81157 conserved hypothetical protein NMB0796 [Imported] - Neisseria meningitidis (strain MC58) serogroup B, strain 22491 serogroup A) gb|AAFE41209.1| conserved hypothetical protein [Neisseria meningitidis MC58] embl|CAB84274.1| hypothetical protein NMA1005 [Neisseria meningitidis 22491] Length = 92

4768.1 Best-BlastP=> >nrprot 52% Identities = 35/101 (34%), Positives = 62/101 (61%), Gaps = 12/101 (11%) ref|ZP_00022930.1| COG2913: Small protein A (tmRNA-binding) [Ralstonia metallidurans] Length = 159

4769.1 Best-BlastP=> >nrprot 99% Identities = 135/136 (99%), Positives = 136/136 (100%) sp|Q48835|FUR LEGPN Ferric uptake regulation protein (Ferric uptake regulator) 9b|AA19656.1| Fur Length = 136

4770.1 Best-BlastP=> >nrprot 68% Identities = 25/46 (54%), Positives = 33/46 (71%), Gaps = 3/46 (6%) emb|CAB87569.1| FldC protein [Sphingomonas sp. LB126] Length = 533

4771.2 Best-BlastP=> >nrprot 26% Identities = 65/166 (39%), Positives = 94/166 (56%), Gaps = 7/166 (4%) ref|NP_907052.1| COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wolinella succinogenes] emb|CAE09952.1| COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wolinella succinogenes] Length = 407

4773.3 Best-BlastP=> >nrprot 77% Identities = 292/461 (63%), Positives = 362/461 (78%) ref|ZP_00015785.1| hypothetical protein [Rhodospirillum rubrum] sp|Q59765|PNTB_RHORU NAD(P) transhydrogenase subunit beta (Pyridine nucleotide transhydrogenase subunit beta) (Nicotinamide nucleotide transhydrogenase subunit beta) (Proton-translocating transhydrogenase NAD(P)-binding component) (dIII) gb|AAC43257.1| nicotinamide nucleotide transhydrogenase, subunit beta gb|AAA62495.1| proton-translocating nicotinamide nucleotide transhydrogenase subunit PntB prfl|2102322C energy-transducing nicotinamide nucleotide transhydrogenase: Length = 464

4774.1 Best-BlastP=> >nrprot 74% Identities = 61/91 (67%), Positives = 74/91 (81%) ref|NP_840934.1| probable transmembrane NAD(P) transhydrogenase (alpha subunit part 2) [Nitrosomonas europaea ATCC 19718] emb|CAD84771.1| probable transmembrane NAD(P) transhydrogenase (alpha subunit part 2) [Nitrosomonas europaea ATCC 19718] Length = 102

4775.2 Best-BlastP=> >nrprot 66% Identities = 179/361 (49%), Positives = 250/361 (69%), Gaps = 9/361 (2%) ref|NP_840933.1| Alanine dehydrogenase and pyridine nucleotide transhydrogenase [Nitrosomonas europaea ATCC 19718] emb|CAD84770.1| Alanine dehydrogenase and pyridine nucleotide transhydrogenase [Nitrosomonas europaea ATCC 19718] Length = 375

4776.3 Best-BlastP=>>nrprot 51% Identities = 59/146 (40%), Positives = 89/146 (60%), Gaps = 8/146 (5%) ref[ZP_00111831.1] COG2340: Uncharacterized protein with SCP/PR1 domains [Nostoc punctiforme] Length = 182

4777.2 Best-BlastP=>>nrprot No Hits found

4778.1 Best-BlastP=>>nrprot No Hits found

4779.1 Best-BlastP=>>nrprot 62% Identities = 68/152 (44%), Positives = 93/152 (61%), Gaps = 4/152 (2%) ref[ZP_00125177.1] COG2153: Predicted acyltransferase [Pseudomonas syringae pv. syringae B728a] Length = 152

4780.2 Best-BlastP=>>nrprot No Hits found

4782.3 Best-BlastP=>>nrprot 99% Identities = 359/363 (98%), Positives = 362/363 (99%) emb[CAB65197.1] hypothetical protein [Legionella pneumophila] Length = 363

4785.1 Best-BlastP=>>nrprot No Hits found

4786.2 Best-BlastP=>>nrprot 52% Identities = 159/409 (38%), Positives = 250/409 (61%), Gaps = 8/409 (1%) ref[NP_819388.1] d-xylose-proton symporter, putative [Coxiella burnetii RSA 493] gb[AAO89902.1] d-xylose-proton symporter, putative [Coxiella burnetii RSA 493] Length = 409

4788.3 Best-BlastP=>>nrprot 98% Identities = 200/204 (98%), Positives = 201/204 (98%) spl[P50024|DSBA_LEGPN THIOL:DISULFIDE INTERCHANGE PROTEIN DSBA PRECURSOR gb[AAA67725.1] disulfide bond forming protein Length = 204

4790.3 Best-BlastP=>>nrprot 77% Identities = 278/425 (65%), Positives = 336/425 (79%), Gaps = 1/425 (0%) ref[NP_820750.1] ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] gb[AAO91264.1] ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] Length = 432

4791.3 Best-BlastP=>>nrprot 35% Identities = 37/91 (40%), Positives = 47/91 (51%) pir[A71007 hypothetical protein PH1351 - Pyrococcus horikoshii dbj|BA30457.1|101aa long hypothetical protein [Pyrococcus horikoshii] Length = 101

4793.2 Best-BlastP=>>nrprot 75% Identities = 306/545 (56%), Positives = 412/545 (75%) ref[NP_820751.1] ABC transporter, permease protein [Coxiella burnetii RSA 493] gb[AAO91265.1] ABC transporter, permease protein [Coxiella burnetii RSA 493] Length = 581

4795.1 Best-BlastP=>>nrprot No Hits found

4796.1 Best-BlastP=>>nrprot 25% Identities = 24/70 (34%), Positives = 36/70 (51%), Gaps = 12/70 (17%) ref[NP_650587.1] CG5225-PA [Drosophila melanogaster] gb[AAF55377.2] CG5225-PA [Drosophila melanogaster] Length = 594

4797.1 Best-BlastP=>>nrprot 91% Identities = 293/351 (83%), Positives = 324/351 (92%) ref[NP_820537.1] ribonucleoside-diphosphate reductase, beta subunit [Coxiella burnetii RSA 493] gb[AAO91051.1] ribonucleoside-diphosphate reductase, beta subunit [Coxiella burnetii RSA 493] Length = 401

48.1 Best-BlastP=>>nrprot 98% Identities = 90/93 (96%), Positives = 93/93 (100%) emb[CAB60052.1] Legionella pneumophila] Length = 93

480.3 Best-BlastP=>>nrprot 88% Identities = 373/475 (78%), Positives = 428/475 (90%), Gaps = 1/475 (0%) ref[NP_820349.1] conserved hypothetical protein [Coxiella burnetii RSA 493] gb[AAO90863.1] conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 480

4800.2 Best-BlastP=>>nrprot 61% Identities = 102/252 (40%), Positives = 160/252 (63%), Gaps = 1/252 (0%) ref[ZP_00110131.1] COG0300: Short-chain dehydrogenases of various substrate specificities [Nostoc punctiforme] Length = 270

4801.1 Best-BlastP=>>nrprot 33% Identities = 31/122 (25%), Positives = 56/122 (45%), Gaps = 24/122 (19%) ref|ZP_00026008.1| COG4970: Tfp pilus assembly protein FimT [Ralstonia metallidurans] Length = 222

4802.2 Best-BlastP=>>nrprot 31% Identities = 34/110 (30%), Positives = 56/110 (50%), Gaps = 7/110 (6%) ref|ZP_00030895.1| COG3161: 4-hydroxybenzoate synthetase (chorismate lyase) [Burkholderia fungorum] Length = 227

4803.2 Best-BlastP=>>nrprot 79% Identities = 148/247 (59%), Positives = 197/247 (79%) ref|NP_793605.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57300.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Pseudomonas syringae pv. tomato str. DC3000] Length = 247

4804.1 Best-BlastP=>>nrprot 84% Identities = 65/73 (89%), Positives = 70/73 (95%) pir|T12021 acyl carrier protein - Pseudomonas aeruginosa gb|AB94392.1| acyl carrier protein [Pseudomonas aeruginosa] Length = 78

4805.1 Best-BlastP=>>nrprot 78% Identities = 258/411 (62%), Positives = 325/411 (79%) ref|NP_251655.1| beta-ketoacyl-acyl carrier protein synthase II [Pseudomonas aeruginosa PA01] pir|T12022 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Pseudomonas aeruginosa gb|AAB94396.1| 3-oxoacyl-acyl carrier protein synthase II [Pseudomonas aeruginosa] gb|AAG06353.1|AE004722_9 beta-ketoacyl-acyl carrier protein synthase II [Pseudomonas aeruginosa PA01] Length = 414

4806.4 Best-BlastP=>>nrprot 60% Identities = 127/330 (38%), Positives = 200/330 (60%), Gaps = 14/330 (4%) ref|NP_819532.1| conserved hypothetical protein TIGR00247 [Coxiella burnetii RSA 493] gb|AAO90046.1| conserved hypothetical protein TIGR00247 [Coxiella burnetii RSA 493] Length = 370

4809.2 Best-BlastP=>>nrprot 46% Identities = 85/287 (29%), Positives = 130/287 (45%), Gaps = 15/287 (5%) ref|ZP_00013543.1| hypothetical protein [Rhodospirillum rubrum] Length = 352

481.1 Best-BlastP=>>nrprot 57% Identities = 62/150 (41%), Positives = 88/150 (58%) ref|NP_2998766.1| conserved hypothetical protein [Xylella fastidiosa 9a5c] pir|H82676 conserved hypothetical protein XF1477 [Imported] - Xylella fastidiosa (strain 9a5c) gb|AAF84286.1|AE003977_9 conserved hypothetical protein [Xylella fastidiosa 9a5c] Length = 153

4810.1 Best-BlastP=>>nrprot No Hits found

4811.2 Best-BlastP=>>nrprot 67% Identities = 89/163 (54%), Positives = 110/163 (67%), Gaps = 1/163 (0%) ref|NP_404518.1| putative membrane protein [Yersinia pestis] pir|AE0110 probable membrane protein YPO0899 [Imported] - Yersinia pestis (strain CO92) embl|CAC89744.1| putative membrane protein [Yersinia pestis CO92] Length = 165

4813.2 Best-BlastP=>>nrprot 63% Identities = 161/389 (41%), Positives = 246/389 (63%), Gaps = 4/389 (1%) gb|AAD47247.1| putative transport protein [Legionella pneumophila] Length = 387

4814.2 Best-BlastP=>>nrprot 65% Identities = 101/199 (50%), Positives = 138/199 (69%), Gaps = 5/199 (2%) ref|NP_820137.1| enhanced entry protein EnhA, putative [Coxiella burnetii RSA 493] gb|AAO90651.1| enhanced entry protein EnhA, putative [Coxiella burnetii RSA 493] Length = 248

4815.2 Best-BlastP=>>nrprot 59% Identities = 56/115 (48%), Positives = 82/115 (71%), Gaps = 1/115 (0%) ref|NP_883806.1| flagellar protein Fls [Bordetella parapertussis] embl|CAE36818.1| flagellar protein Fls [Bordetella parapertussis] Length = 142

4817.4 Best-BlastP=>>nrprot No Hits found

4818.3 Best-BlastP=>>nrprot No Hits found

4819.2 Best-BlastP=>>nrprot 40% Identities = 70/290 (24%), Positives = 129/290 (44%), Gaps = 13/290 (4%) gb|AAF20289.1|AF121266_11 malonyl-CoA:ACP transacylase MdcG [Acinetobacter calcoaceticus] Length = 307

482.2 Best-BlastP=>>nrprot 62% Identities = 257/538 (47%), Positives = 363/538 (67%), Gaps = 9/538 (1%) gb|AAM48100.1|AF353205_1 poly-beta-hydroxybutyrate synthase [Azospirillum brasiliense] Length = 618

4821.2 Best-BlastP=>>nrprot 44% Identities = 79/266 (29%), Positives = 125/266 (46%), Gaps = 34/266 (12%) ref|NP_440042.1| alkaline phosphatase [Synechocystis sp. PCC 6803] pir|S74570 alkaline phosphatase (EC 3.1.3.1) phoA - Synechocystis sp. (strain PCC 6803) Length = 326

4822.3 Best-BlastP=>>nrprot 35% Identities = 73/276 (26%), Positives = 119/276 (43%), Gaps = 37/276 (13%) ref|ZP_00123112.1| hypothetical protein [Haemophilus somnus 129PT] Length = 308

4826.2 Best-BlastP=>>nrprot 49% Identities = 64/203 (31%), Positives = 115/203 (56%), Gaps = 11/203 (5%) ref|NP_819961.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AO90475.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 227

4830.2 Best-BlastP=>>nrprot 26% Identities = 39/135 (28%), Positives = 80/135 (59%) ref|ZP_00060561.1| hypothetical protein [Clostridium thermocellum ATCC 27405] Length = 902

4833.2 Best-BlastP=>>nrprot 33% Identities = 44/162 (27%), Positives = 85/162 (52%), Gaps = 4/162 (2%) ref|NP_149698.1| 235L [Invertebrate iridescent virus 6] gb|AAK82096.1|AF303741_235L [Chilo iridescent virus] Length = 265

4834.4 Best-BlastP=>>nrprot No Hits found

4835.4 Best-BlastP=>>nrprot 67% Identities = 101/174 (58%), Positives = 135/174 (77%) ref|ZP_00126146.1| COG1187: 16S rRNA uridine-5'16 pseudouridylate synthase and related pseudouridylate synthases [Pseudomonas syringae pv. syringae B728a] Length = 210

4836.1 Best-BlastP=>>nrprot 48% Identities = 45/135 (33%), Positives = 79/135 (58%) ref|NP_743096.1| rod shape-determining protein MreD [Pseudomonas putida KT2440] gb|AAN66560.1|AE016284_8 rod shape-determining protein MreD [Pseudomonas putida KT2440] Length = 163

4837.1 Best-BlastP=>>nrprot 63% Identities = 116/273 (42%), Positives = 178/273 (65%), Gaps = 3/273 (1%) ref|NP_820453.1| rod shape-determining protein MreC [Coxiella burnetii RSA 493] gb|AO90967.1| rod shape-determining protein MreC [Coxiella burnetii RSA 493] Length = 292

4841.2 Best-BlastP=>>nrprot 92% Identities = 287/348 (82%), Positives = 320/348 (91%), Gaps = 3/348 (0%) ref|NP_820454.1| rod shape-determining protein MreB [Coxiella burnetii RSA 493] gb|AO90968.1| rod shape-determining protein MreB [Coxiella burnetii RSA 493] Length = 352

4844.2 Best-BlastP=>>nrprot No Hits found

4845.4 Best-BlastP=>>nrprot 22% Identities = 67/290 (23%), Positives = 129/290 (44%), Gaps = 34/290 (11%) ref|ZP_00036809.1| COG0419: ATPase involved in DNA repair [Enterococcus faecium] Length = 1042

4847.2 Best-BlastP=>>nrprot No Hits found

4848.3 Best-BlastP=>>nrprot 52% Identities = 116/301 (38%), Positives = 178/301 (59%), Gaps = 1/301 (0%) ref|ZP_00053871.1| COG0845: Membrane-fusion protein [Magnetospirillum magnetotacticum] Length = 335

485.3 Best-BlastP=>>nrprot 41% Identities = 106/439 (24%), Positives = 199/439 (45%), Gaps = 41/439 (9%) ref|NP_932208.1| putative conjugative transfer protein TrAB [Vibrio vulnificus] YJ016] Length = 603

4850.2 Best-BlastP=>>nrprot No Hits found

4851.2 Best-BlastP=>>nrprot 67% Identities = 89/161 (55%), Positives = 109/161 (67%), Gaps = 2/161 (1%) ref|ZP_00054128.1| COG3837: Uncharacterized conserved protein, contains double-stranded beta-helix domain [Magnetospirillum magnetotacticum] Length = 180

4855.2 Best-BlastP=>>nrprot 80% Identities = 67/91 (73%), Positives = 79/91 (86%) ref|NP_717690.1| integration host factor, alpha subunit [Shewanella oneidensis] MR-1] gb|AAN55134.1|AE015650_4 integration host factor, alpha subunit [Shewanella oneidensis] MR-1] Length = 98

4856.2 Best-BlastP=>>nrprot 67% Identities = 51/100 (51%), Positives = 72/100 (72%) ref|NP_841896.1| putative ferredoxin 2fe-2s protein [Nitrosomonas europaea ATCC 19718] emb|CAD85785.1| putative ferredoxin 2fe-2s protein [Nitrosomonas europaea ATCC 19718]

4859.2 Best-BlastP=>>nrprot No Hits found

486.2 Best-BlastP=>>nrprot No Hits found

4860.1 Best-BlastP=>>nrprot No Hits found

4863.4 Best-BlastP=>>nrprot 69% Identities = 220/430 (51%), Positives = 294/430 (68%), Gaps = 13/430 (3%) ref|NP_406861.1| poly(A) polymerase [Yersinia pestis] pir|A|0412 polynucleotide adenylyltransferase (EC 2.7.19) [imported] - Yersinia pestis (strain CO92) emb|CAC92629.1| poly(A) polymerase [Yersinia pestis CO92] Length = 440

4864.2 Best-BlastP=>>nrprot 66% Identities = 62/131 (47%), Positives = 88/131 (67%) ref|NP_735626.1| Unknown [Streptococcus agalactiae NEM316] emb|CAD46839.1| Unknown [Streptococcus agalactiae NEM316] Length = 162

4865.2 Best-BlastP=>>nrprot 58% Identities = 48/146 (32%), Positives = 83/146 (56%), Gaps = 12/146 (8%) ref|NP_841101.1| Universal stress protein (Usp) [Nitrosomonas europaea ATCC 19718] emb|CAD84939.1| Universal stress protein (Usp) [Nitrosomonas europaea ATCC 19718] Length = 148

4867.2 Best-BlastP=>>nrprot 62% Identities = 209/445 (46%), Positives = 293/445 (65%), Gaps = 3/445 (0%) ref|ZP_00025176.1| COG1012: NAD-dependent aldehyde dehydrogenases [Ralstonia metallidurans] Length = 520

4868.2 Best-BlastP=>>nrprot 72% Identities = 155/269 (57%), Positives = 197/269 (73%), Gaps = 1/269 (0%) pir|T34105 hypothetical protein C17G10.8 - Caenorhabditis elegans Length = 938

4869.3 Best-BlastP=>>nrprot 75% Identities = 90/139 (64%), Positives = 108/139 (77%) ref|NP_540374.1| RIBONUCLEASE HI [Brucella melitensis] ref|NP_697505.1| ribonuclease H [Brucella suis 1330] sp|Q8YF3|RNH_BRUME Ribonuclease H (RNase H) pir|AC3434 calf thymus ribonuclease H (EC 3.1.26.4) [imported] - Brucella melitensis (strain 16M) gb|AAL52638.1| RIBONUCLEASE HI [Brucella melitensis 16M] Length = 154

4872.3 Best-BlastP=>>nrprot 98% Identities = 511/520 (98%), Positives = 515/520 (99%) gb|AAM00608.1| unknown [Legionella pneumophila] Length = 520

4873.3 Best-BlastP=>>nrprot 99% Identities = 383/387 (98%), Positives = 385/387 (99%) gb|AAM00609.1| unknown [Legionella pneumophila] Length = 388

4874.2 Best-BlastP=>>nrprot 41% Identities = 108/445 (24%), Positives = 193/445 (43%), Gaps = 79/445 (17%) ref|NP_621958.1| ATPase involved in DNA repair [Thermoanaerobacter tengcongensis] gb|AM23562.1| ATPase involved in DNA repair [Thermoanaerobacter tengcongensis] Length = 1177

4875.1 Best-BlastP=>>nrprot 69% Identities = 73/119 (61%), Positives = 91/119 (76%), Gaps = 6/119 (5%) ref|ZP_00033092.1| COG0316: Uncharacterized conserved protein [Burkholderia fungorum] Length = 121

4877.2 Best-BlastP=>>nrprot 74% Identities = 202/356 (56%), Positives = 269/356 (75%), Gaps = 1/356 (0%) ref|NP_746144.1| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Pseudomonas putida KT2440] gb|AAN69608.1|AE016594_5 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Pseudomonas putida KT2440] Length = 374

4878.2 Best-BlastP=>>nrprot 54% Identities = 161/418 (38%), Positives = 242/418 (57%), Gaps = 6/418 (1%) ref|ZP_00086772.1| COG0739: Membrane proteins related to metalloendopeptidases [Pseudomonas fluorescens PRO-1] Length = 471

488.2 Best-BlastP=>>nrprot 75% Identities = 181/298 (60%), Positives = 230/298 (77%) ref|ZP_000683320.1| COG1131: ABC-type multidrug transport system, ATPase component [Microbulbifer degradans 2-40] Length = 318

4880.2 Best-BlastP=>>nrprot 49% Identities = 92/270 (34%), Positives = 136/270 (50%), Gaps = 9/270 (3%) ref|NP_085189.1| IS10 of [Shigella flexneri] ref|NP_858160.1| hypothetical protein [Shigella flexneri 2a] gb|AAK18345.1|AF348706_34 [S10 of [Shigella flexneri] gb|AAL72480.1| hypothetical protein [Shigella flexneri 2a] Length = 407

4881.4 Best-BlastP=>>nrprot 11% Identities = 72/284 (25%), Positives = 121/284 (42%), Gaps = 19/284 (6%) ref|ZP_00112010.1| hypothetical protein [Nostoc punctiforme] Length = 427

4883.2 Best-BlastP=>>nrprot 50% Identities = 45/105 (42%), Positives = 67/105 (63%), Gaps = 1/105 (0%) ref|NP_819268.1| preprotein translocase, SecE subunit [Coxiella burnetii RSA 493] gb|AAO89782.1| preprotein translocase, SecE subunit [Coxiella burnetii RSA 493] Length = 127

4884.1 Best-BlastP=>>nrprot 80% Identities = 125/175 (71%), Positives = 148/175 (84%) ref|ZP_00123792.1| COG0250: Transcription antiterminator [Pseudomonas syringae pv. syringae B728a] ref|NP_790461.1| transcription antitermination protein NusG [Pseudomonas syringae pv. tomato str. DC3000] gb|DC3000| transcription antitermination protein NusG [Pseudomonas syringae pv. tomato str. DC3000] Length = 177

4885.2 Best-BlastP=>>nrprot 87% Identities = 112/143 (78%), Positives = 127/143 (88%) ref|NP_282996.1| 50S ribosomal protein L11 [Neisseria meningitidis Z2491] pir|H82007 50S ribosomal protein L11 NMA0146 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) Length = 144

4887.3 Best-BlastP=>>nrprot 57% Identities = 72/176 (40%), Positives = 102/176 (57%), Gaps = 6/176 (3%) ref|NP_419908.1| acetyltransferase, GNAT family [Caulobacter crescentus CB15] pir|H87384 acetyltransferase, GNAT family [imported] - Caulobacter crescentus gb|AAK23076.1| acetyltransferase, GNAT family [Caulobacter crescentus CB15] Length = 181

4888.1 Best-BlastP=>>nrprot 59% Identities = 63/151 (41%), Positives = 103/151 (68%) emb|CAD31280.1| PUTATIVE TRANSCRIPTION REGULATOR PROTEIN [Mesorhizobium loti] Length = 151

4889.1 Best-BlastP=>>nrprot 49% Identities = 44/120 (36%), Positives = 66/120 (55%), Gaps = 3/120 (2%) ref|NP_819252.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89766.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 130

489.1 Best-BlastP=>>nrprot No Hits found

4891.2 Best-BlastP=>>nrprot 26% Identities = 39/138 (28%), Positives = 67/138 (48%), Gaps = 19/138 (13%) pir||A59234 slow myosin heavy chain 3 - quail gb|AAC59911.1| slow myosin heavy chain 3 gb|AAC59912.1| slow myosin heavy chain 3 Length = 1931

4894.1 Best-BlastP=>>nrprot 69% Identities = 52/121 (42%), Positives = 81/121 (66%), Gaps = 7/121 (5%) ref|NP_746309.1| succinate dehydrogenase, hydrophobic membrane anchor protein [Pseudomonas putida KT2440] gb|AAN89773.1|AE016613_8 succinate dehydrogenase, hydrophobic membrane anchor protein [Pseudomonas putida KT2440] Length = 122

4895.1 Best-BlastP=>>nrprot 69% Identities = 60/124 (48%), Positives = 87/124 (70%) ref|NP_250272.1| succinate dehydrogenase (C subunit) [Pseudomonas aeruginosa PA01] pir||C83448 succinate dehydrogenase (C subunit) PA1581 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AA04970.1|AE004586_8 succinate dehydrogenase (C subunit) [Pseudomonas aeruginosa PAO1] Length = 128

4897.2 Best-BlastP=>>nrprot 47% Identities = 103/370 (27%), Positives = 179/370 (48%), Gaps = 22/370 (5%) ref|NP_761171.1| Predicted signal transduction protein [Vibrio vulnificus CMCP6] gb|AAO11244.1|AE016806_234 Predicted signal transduction protein [Vibrio vulnificus CMCP6] Length = 404

4900.3 Best-BlastP=>>nrprot 41% Identities = 205/972 (21%), Positives = 412/972 (42%), Gaps = 110/972 (11%) ref|NP_245295.1| unknown [Pasteurella multocida] gb|AAK02442.1| unknown [Pasteurella multocida] Length = 1113

4901.3 Best-BlastP=>>nrprot 76% Identities = 357/592 (60%), Positives = 454/592 (76%), Gaps = 1/592 (0%) ref|NP_842254.1| aspartyl-tRNA synthetase [Nitrosomonas europaea ATCC 19718] embl|CAD86164.1| aspartyl-tRNA synthetase [Nitrosomonas europaea ATCC 19718] Length = 593

4902.1 Best-BlastP=>>nrprot 25% Identities = 23/43 (53%), Positives = 28/43 (65%) ref|NP_275122.1| hypothetical protein [Neisseria meningitidis MC58] pir||G81001 hypothetical protein NMB2137 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF42445.1| hypothetical protein [Neisseria meningitidis MC58] Length = 70

4907.2 Best-BlastP=>>nrprot 72% Identities = 134/257 (52%), Positives = 186/257 (72%), Gaps = 9/257 (3%) ref|ZP_00067917.1| COG1054: Predicted sulfuryltransferase [Microbulbifer degradans 2-40] Length = 309

4908.3 Best-BlastP=>>nrprot 58% Identities = 715/1981 (36%), Positives = 1108/1981 (55%), Gaps = 111/1981 (5%) ref|NP_406102.1| putative membrane protein [Yersinia pestis] ref|NP_668470.1| conserved hypothetical protein [Yersinia pestis KIM] sp|Q8ZDJ2|YP73_YERPE Hypothetical UPF0192 protein YP02573/Y1143 precursor pir||AC0314 probable membrane protein YPO2573 [imported] - Yersinia pestis embl|CAC91375.1| putative membrane protein [Yersinia pestis CO92] gb|AAM84721.1|AE013717_3 conserved hypothetical protein [Yersinia pestis KIM] Length = 2004

491.1 Best-BlastP=>>nrprot 34% Identities = 62/271 (22%), Positives = 116/271 (42%), Gaps = 20/271 (7%) sp|O60610|DIA1_HUMAN Diaphanous protein homolog 1 (Diaphanous-related formin 1) (DRF1) gb|AAC053373.1| diaphanous 1 [Homo sapiens] Length = 1248

4913.2 Best-BlastP=>>nrprot No Hits found

4914.2 Best-BlastP=>>nrprot No Hits found

4916.2 Best-BlastP=>>nrprot 30% Identities = 53/186 (28%), Positives = 93/186 (50%), Gaps = 11/186 (5%) ref|NP_179611.1| leucine rich repeat protein family [Arabidopsis thaliana] pir||D84586 hypothetical protein At2g20210 [imported] - Arabidopsis thaliana gb|AAD21766.1| hypothetical protein [Arabidopsis thaliana] Length = 271

4917.2 Best-BlastP=>>nrprot No Hits found

4918.2 Best-BlastP=>>nrprot 17% Identities = 31/114 (27%), Positives = 52/114 (45%), Gaps = 4/114 (3%) ref|NP_281741.1| putative integral membrane protein [Campylobacter jejuni] pir|E81402 probable integral membrane protein Cj0557c [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB75193.1| putative integral membrane protein [Campylobacter jejuni subsp. jejuni] NCTC 11168] Length = 361

4919.1 Best-BlastP=>>nrprot 44% Identities = 109/421 (25%), Positives = 192/421 (45%), Gaps = 24/421 (5%) ref|NP_900103.1| outer membrane efflux protein [Chromobacterium violaceum ATCC 12472] Length = 466

492.4 Best-BlastP=>>nrprot 59% Identities = 48/101 (47%), Positives = 70/101 (69%), Gaps = 1/101 (0%) ref|NP_761137.1| SM-20-related protein [Vibrio vulnificus CMCP6] gb|AAQ10664.1|AE016804_174 SM-20-related protein [Vibrio vulnificus CMCP6] dbj|BAC94823.1| SM-20-related protein [Vibrio vulnificus YJ016] Length = 200

4920.4 Best-BlastP=>>nrprot 56% Identities = 88/284 (30%), Positives = 143/284 (50%), Gaps = 38/284 (13%) ref|NP_791175.1| sensory box/GGDEF domain/EAL domain protein [Pseudomonas syringae] gb|AAO54870.1| sensory box/GGDEF domain/EAL domain protein [Pseudomonas syringae] pv. tomato str. DC3000] Length = 763

4923.2 Best-BlastP=>>nrprot 79% Identities = 433/634 (68%), Positives = 507/634 (79%) ref|ZP_00066531.1| COG0441: Threonyl-tRNA synthetase [Microbulifer degradans 2-40] Length = 636

4927.1 Best-BlastP=>>nrprot No Hits found

4929.2 Best-BlastP=>>nrprot 72% Identities = 164/298 (55%), Positives = 223/298 (74%), Gaps = 2/298 (0%) ref|NP_622015.1| uncharacterized enzyme involved in pigment biosynthesis [Thermoanaerobacter tengcongensis] gb|AAM23619.1| uncharacterized enzyme involved in pigment biosynthesis [Thermoanaerobacter tengcongensis] Length = 307

493.4 Best-BlastP=>>nrprot 55% Identities = 83/216 (38%), Positives = 131/216 (60%) ref|NP_634315.1| Zinc metalloprotease [Methanoscarcina mazei Goe1] gb|AAM31987.1| Zinc metalloprotease [Methanoscarcina mazei Goe1] Length = 238

4930.2 Best-BlastP=>>nrprot 78% Identities = 51/90 (56%), Positives = 71/90 (78%) ref|NP_819953.1| conserved hypothetical protein [Coxiella burnetii RSA 493] sp|Q83D06|Y941_COXBU Hypothetical UPF0269 protein CBU0941 gb|AAO90467.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 90

4934.3 Best-BlastP=>>nrprot 26% Identities = 59/198 (29%), Positives = 101/198 (51%), Gaps = 27/198 (13%) ref|NP_628263.1| possible secreted peptidase [Streptomyces coelicolor A3(2)] emb|CAB56362.1| possible secreted peptidase [Streptomyces coelicolor A3(2)] Length = 279

4935.2 Best-BlastP=>>nrprot 63% Identities = 168/345 (48%), Positives = 225/345 (65%) ref|NP_216774.1| hypothetical protein Rv2258c [Mycobacterium tuberculosis H37Rv] ref|NP_336787.1| methyltransferase-related protein [Mycobacterium tuberculosis subsp. bovis AF2122/97] pnt|F70862 probable helix-turn helix motif at aa 47-68 - Mycobacterium tuberculosis (strain H37RV) emb|CAA17295.1| hypothetical protein Rv2258c [Mycobacterium tuberculosis H37Rv] gb|AAK46601.1| methyltransferase-related protein [Mycobacterium tuberculosis subsp. bovis AF2122/97] emb|CAD97135.1| Possible transcriptional regulatory protein [Mycobacterium bovis] Length = 353

494.2 Best-BlastP=>>nrprot 75% Identities = 160/283 (56%), Positives = 212/283 (74%), Gaps = 5/283 (1%) ref|NP_518195.1| PROBABLE METALLOPROTEASE ZINC TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] sp|Q8Y3A6|HTPX_RALSO Probable protease htpX homolog emb|CAD13602.1| PROBABLE METALLOPROTEASE ZINC TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 286

4941.2 Best-BlastP=>>nrprot No Hits found

4942.1 Best-BlastP=>>nrprot No Hits found

4943.2 Best-BlastP=>>nrprot No Hits found

4945.2 Best-BlastP=>>nrprot 79% Identities = 214/340 (62%), Positives = 268/340 (78%), Gaps = 11/340 (3%) ref|NP_052843.1| hypothetical protein [Coxiella burnetii] ref|NP_819053.1| repB protein, putative [Coxiella burnetii RSA 493] pir|S552723 qsopB protein - Coxiella burnetii plasmid QpH1 gb|AA69865.1| qsopB gene product emb|CAA59788.1| orf 334 [Coxiella burnetii] emb|CAA75818.1| hypothetical protein [Coxiella burnetii] gbi|AAD33475.1|AF131076_1 hypothetical protein [Coxiella burnetii] gbi|AAO91613.1| repB protein, putative [Coxiella burnetii RSA 493] prf|2117254B trans-acting factor Length = 334

4947.2 Best-BlastP=>>nrprot 93% Identities = 340/402 (84%), Positives = 377/402 (93%) ref|NP_052336.1| unnamed protein product [Coxiella burnetii] ref|NP_052844.1| hypothetical protein [Coxiella burnetii] ref|NP_819052.1| parA protein, putative [Coxiella burnetii RSA 493] pir|S68866 qsopA protein - Coxiella burnetii plasmid QpH1 emb|CAA53106.1| unnamed protein product [Coxiella burnetii] gbi|AA69864.1| qsopA gene product emb|CAA59789.1| orf 406 [Coxiella burnetii] emb|CAA75819.1| putative SopA protein (protein a) [Coxiella burnetii] gbi|ADD33476.1|AF131076_2 hypothetical protein [Coxiella burnetii] gbi|AAO91612.1| parA protein, putative [Coxiella burnetii RSA 493] prf|2117254A trans-acting factor Length = 406

4948.4 Best-BlastP=>>nrprot No Hits found

4951.2 Best-BlastP=>>nrprot 24% Identities = 25/79 (31%), Positives = 40/79 (50%), Gaps = 4/79 (5%) ref|ZP_00103190.1| COG1396: Predicted transcriptional regulators [Desulfitobacterium hafniense] Length = 123

4952.1 Best-BlastP=>>nrprot No Hits found

4954.2 Best-BlastP=>>nrprot 53% Identities = 62/155 (40%), Positives = 92/155 (59%) ref|NP_746668.1| polypeptide deformylase [Pseudomonas putida KT2440] sp|Q88EA7|DEF2_PSEPK Peptide deformylase 2 (PDF 2) (Polypeptide deformylase 2) gbi|AAN70132.1|AE016653_3 polypeptide deformylase [Pseudomonas putida KT2440] Length = 178

4955.4 Best-BlastP=>>nrprot 50% Identities = 132/417 (31%), Positives = 218/417 (52%), Gaps = 9/417 (2%) ref|NP_221200.1| PROLINE/BETAINE TRANSPORTER (prop6) [Rickettsia prowazekii] pir|D71647 proline/betaine transporter (prop6) RP852 - Rickettsia prowazekii emb|CAA15276.1| PROLINE/BETAINE TRANSPORTER (prop6) [Rickettsia prowazekii] Length = 415

4957.2 Best-BlastP=>>nrprot 62% Identities = 53/108 (49%), Positives = 74/108 (68%), Gaps = 3/108 (2%) ref|NP_251650.1| type 4 fimbrial biogenesis protein PilZ [Pseudomonas aeruginosa PA01] pir|IB59241 type 4 fimbriae biogenesis protein [imported] - Pseudomonas aeruginosa gbi|AA93519.1| involved in biogenesis of type 4 fimbriae gbi|AAG06348.1|AE004722_4 type 4 fimbrial biogenesis protein PilZ [Pseudomonas aeruginosa PA01] Length = 118

4958.3 Best-BlastP=>>nrprot 47% Identities = 90/313 (28%), Positives = 142/313 (45%), Gaps = 20/313 (6%) ref|NP_819534.1| DNA polymerase III, delta prime subunit [Coxiella burnetii RSA 493] gbi|AAO90048.1| DNA polymerase III, delta prime subunit [Coxiella burnetii RSA 493] Length = 319

496.1 Best-BlastP=>>nrprot No Hits found

4960.2 Best-BlastP=> >nrprot No Hits found

4961.1 Best-BlastP=> >nrprot 77% Identities = 70/127 (55%), Positives = 99/127 (77%), Gaps = 4/127 (3%) ref|NP_391517.1| similar to large conductance mechanosensitive channel protein [Bacillus subtilis] sp|P94585|MSCL_BACSU Large-conductance mechanosensitive channel pir||E70065 large conductance mechanosensitive channel homolog ywpc - Bacillus subtilis emb|CAB05944.1| ywpc [Bacillus subtilis] emb|CAB15653.1| large conductance mechanosensitive channel protein [Bacillus subtilis subsp. subtilis str. 168] Length = 130

4962.2 Best-BlastP=> >nrprot No Hits found

4965.2 Best-BlastP=> >nrprot 61% Identities = 99/105 (94%), Positives = 102/105 (97%) emb|CAB65201.1| hypothetical protein [Legionella pneumophila] Length = 356

4966.2 Best-BlastP=> >nrprot 98% Identities = 586/598 (97%), Positives = 590/598 (98%) emb|CAB65200.1| hypothetical protein [Legionella pneumophila] Length = 598

4968.2 Best-BlastP=> >nrprot 63% Identities = 60/128 (46%), Positives = 83/128 (64%) ref|NP_439721.1| alanine racemase biosynthetic [Haemophilus influenzae Rd] sp|P45257|ALR_HAEIN Alanine racemase pir||E64130 alanine racemase (EC 5.1.1.1), biosynthetic - Haemophilus influenzae (strain Rd KW20) gb|AAC23218.1| alanine racemase, biosynthetic (alr) [Haemophilus influenzae Rd] Length = 360

4969.3 Best-BlastP=> >nrprot 81% Identities = 117/163 (71%), Positives = 141/163 (86%), Gaps = 1/163 (0%) ref|NP_719448.1| replicative DNA helicase [Shewanella oneidensis MR-1] gb|AN56892.1|AE015824_3 replicative DNA helicase [Shewanella oneidensis MR-1] Length = 468

4971 Best-BlastP=> >nrprot No Hits found

4972.3 Best-BlastP=> >nrprot 68% Identities = 111/195 (56%), Positives = 146/195 (74%) ref|ZP_00091033.1| COG0305: Replicative DNA helicase [Azotobacter vinelandii] Length = 463

4974.1 Best-BlastP=> >nrprot 40% Identities = 43/138 (31%), Positives = 71/138 (51%), Gaps = 6/138 (4%) pir||T18332 icml protein - Legionella pneumophila gb|AAC38190.1| Dotl [Legionella pneumophila] emb|CAA75329.1| icml protein [Legionella pneumophila] emb|CAD43145.1| Dotl protein [Legionella pneumophila serogroup 6] Length = 212

4977.3 Best-BlastP=> >nrprot No Hits found

4979.1 Best-BlastP=> >nrprot 71% Identities = 115/192 (59%), Positives = 144/192 (75%) ref|NP_246450.1| unknown [Pasteurella multocida] sp|P57947|ENGB_PASMU Probable GTP-binding protein engB gb|AAK03595.1| unknown [Pasteurella multocida] Length = 205

498.4 Best-BlastP=> >nrprot 37% Identities = 78/305 (25%), Positives = 125/305 (40%), Gaps = 56/305 (18%) ref|NP_421401.1| amine oxidase, flavin-containing [Caulobacter crescentus CB15] pir||E87571 amine oxidase, flavin-containing [Imported] - Caulobacter crescentus gbi|AK24569.1| amine oxidase, flavin-containing [Caulobacter crescentus CB15] Length = 454

4980.3 Best-BlastP=> >nrprot 69% Identities = 102/206 (49%), Positives = 139/206 (67%), Gaps = 7/206 (3%) ref|NP_759874.1| Cytochrome c4 [Vibrio vulnificus CMCP6] gbi|AAQ09401.1|AE016800_6 Cytochrome c4 [Vibrio vulnificus CMCP6] Length = 205

4984.2 Best-BlastP=> >nrprot 73% Identities = 109/166 (65%), Positives = 126/166 (75%), Gaps = 1/166 (0%) gbi|AAO38281.1| Lfe115p1 [Leptospirillum ferrooxidans] Length = 178

4987.2 Best-BlastP=> >nprot 77% Identities = 274/490 (55%), Positives = 360/490 (73%), Gaps = 28/490 (5%) ref|NP_457051.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP_804211.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] spt|Q8Z4P6|ENGA_SALTI Probable GTP-binding protein engA pir|AF0821 probable GTP-binding protein STY2764 [Imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18) emb|CAD02722.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO68060.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 490

499.2 Best-BlastP=> >nprot 51% Identities = 129/343 (37%), Positives = 196/343 (57%), Gaps = 10/343 (2%) ref|ZP_00106589.1| COG1680: Beta-lactamase class C and other penicillin binding proteins [Nostoc punctiforme] Length = 393

4990.3 Best-BlastP=> >nprot No Hits found

4992.2 Best-BlastP=> >nprot 36% Identities = 44/89 (49%), Positives = 63/89 (70%) ref|ZP_00102874.1| hypothetical protein [Desulfitobacterium hafniense] Length = 106

4993.2 Best-BlastP=> >nprot 36% Identities = 44/89 (49%), Positives = 63/89 (70%) ref|ZP_00102874.1| hypothetical protein [Desulfitobacterium hafniense] Length = 106

4995.1 Best-BlastP=> >nprot 33% Identities = 42/179 (23%), Positives = 73/179 (40%), Gaps = 36/179 (20%) ref|NP_229450.1| alpha-amylase, putative [Thermotoga maritima] pir|G72227 hypothetical protein TM1650 - Thermotoga maritima (strain MSB8) gb|AAD36717.1|AE001807_8

4998.2 Best-BlastP=> >nprot 16% Identities = 47/200 (23%), Positives = 87/200 (43%), Gaps = 16/200 (8%) ref|NP_036450.1| leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens] gb|AAD13138.1| leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens] gb|AAH21208.1| Leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens] Length = 422

4999.2 Best-BlastP=> >nprot 77% Identities = 157/241 (65%), Positives = 197/241 (81%), Gaps = 4/241 (1%) ref|NP_252346.1| 30S ribosomal protein S2 [Pseudomonas aeruginosa PA01] sp|O82850|RS2_PSEAE 30S ribosomal protein S2 pir|C83189 30S ribosomal protein S2 PA3656 [Imported] - *Pseudomonas aeruginosa* (strain PAO1) gb|AG07044.1|AE004785_8 30S ribosomal protein S2 [Pseudomonas aeruginosa PAO1] Length = 246

50.1 Best-BlastP=> >nprot 84% Identities = 76/92 (82%), Positives = 80/92 (86%) emb|CAB60051.1| lvhB2 [Legionella pneumophila] gb|AM08238.1| putative pilin subunit [Legionella pneumophila] Length = 96

500.2 Best-BlastP=> >nprot 97% Identities = 341/352 (96%), Positives = 346/352 (98%) gb|AAQ59860.1|AF299349_1 major acid phosphatase [Legionella pneumophila] Length = 352

5000.3 Best-BlastP=> >nprot 97% Identities = 131/136 (96%), Positives = 134/136 (98%) emb|CAB09802.1| 16 kD immunogenic protein [Legionella pneumophila] Length = 136

5001.1 Best-BlastP=> >nprot No Hits found

5003.2 Best-BlastP=> >nprot No Hits found

5005.3 Best-BlastP=> >nprot 99% Identities = 454/455 (99%), Positives = 455/455 (100%) gb|AAQ18124.1| CpxA [Legionella pneumophila] Length = 455

501.2 Best-BlastP=> >nprot 30% Identities = 40/167 (23%), Positives = 75/167 (44%), Gaps = 13/167 (7%) db|BAC45194.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)] Length = 1967

5010.2 Best-BlastP=>>nrprot 18% Identities = 34/1117 (29%), Positives = 54/1117 (46%), Gaps = 12/1117 (10%) emb|CAD90592.1| C3L protein [Cowpox virus] Length = 833

5015.2 Best-BlastP=>>nrprot 58% Identities = 43/1110 (39%), Positives = 66/1110 (60%), Gaps = 3/1110 (2%) ref|ZP_00056081.1| hypothetical protein [Magnetospirillum magnetotacticum] Length = 164

5018.2 Best-BlastP=>>nrprot No Hits found

5019.1 Best-BlastP=>>nrprot 61% Identities = 87/190 (45%), Positives = 125/190 (65%) gb|AAG10504.1|AF279106_66 predicted YacE family of P-loop kinases [uncultured marine gamma proteobacterium EBAC31A08] Length = 197

502.3 Best-BlastP=>>nrprot No Hits found

5021.3 Best-BlastP=>>nrprot 48% Identities = 64/247 (25%), Positives = 120/247 (48%), Gaps = 8/247 (3%) ref|NP_903494.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61486.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 252

5022.2 Best-BlastP=>>nrprot 58% Identities = 124/336 (36%), Positives = 204/336 (60%), Gaps = 5/336 (1%) ref|NP_7425592.1| membrane protein, putative [Pseudomonas putida KT2440] gb|AN66056.1|AE016234_9 membrane protein, putative [Pseudomonas putida KT2440] Length = 346

5026.1 Best-BlastP=>>nrprot 77% Identities = 49/89 (55%), Positives = 70/89 (78%) ref|NP_250138.1| flagellar biosynthetic protein FlIQ [Pseudomonas aeruginosa PA01] ref|ZP_00139064.1| COG1987: Flagellar biosynthesis pathway, component FlIQ [Pseudomonas aeruginosa UCBPP-PA14] pif|A83465 flagellar biosynthetic protein FlIQ PA1447 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG04836.1|AE004574_7 flagellar biosynthetic protein FlIQ [Pseudomonas aeruginosa PAO1] Length = 89

5028.2 Best-BlastP=>>nrprot 70% Identities = 270/528 (51%), Positives = 367/528 (69%), Gaps = 5/528 (0%) ref|NP_820198.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90712.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 550

503.3 Best-BlastP=>>nrprot 55% Identities = 162/399 (40%), Positives = 247/399 (61%), Gaps = 3/399 (0%) ref|ZP_00065233.1| COG0741: Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) Length = 543

5030.2 Best-BlastP=>>nrprot 84% Identities = 225/326 (69%), Positives = 276/326 (84%) ref|NP_820836.1| peptide ABC transporter, permease protein [Coxiella burnetii RSA 493] gb|AAO91350.1| peptide ABC transporter, permease protein [Coxiella burnetii RSA 493] Length = 327

5031.2 Best-BlastP=>>nrprot 40% Identities = 42/173 (24%), Positives = 75/173 (43%), Gaps = 12/173 (6%) ref|NP_542876.1| hypothetical protein [Pseudomonas putida] emb|CAC86816.1| hypothetical protein [Pseudomonas putida] Length = 267

5032.1 Best-BlastP=>>nrprot No Hits found

5033.1 Best-BlastP=>>nrprot No Hits found

5037.1 Best-BlastP=>>nrprot 84% Identities = 35/43 (81%), Positives = 38/43 (88%) ref|NP_300059.1| 50S ribosomal protein L34 [Xylella fastidiosa 9a5c] ref|NP_780293.1| 50S ribosomal protein L34 [Xylella fastidiosa Temecula1] sp|Q9P9T9|RL34_XYLFA 50S ribosomal protein L34 pif|B82517 50S ribosomal protein L34 XF2782 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF85567.1|AE004083_6 50S ribosomal protein L34 [Xylella fastidiosa 9a5c] gb|AAO29942.1| 50S ribosomal protein L34 [Xylella fastidiosa Temecula1] Length = 46

5038.1 Best-BlastP=> nrprot 57% Identities = 45/107 (42%), Positives = 66/107 (61%), Gaps = 2/107 (1%) ref|NP_290337.1| RNase P, protein component; protein C5; processes tRNA, 4.5S RNA [Escherichia coli O157:H7] sp|Q8XB43|RNPA_ECO57 Ribonuclease P protein component [Escherichia coli O157:H7 EDL933] ref|NP_312666.1| ribonuclease P protein (Protein C5) pir||G91208 ribonuclease P protein component [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|A86055 hypothetical protein rnpA [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gb|AAG58901.1|AE005601_7 RNase P, protein component; protein C5; processes tRNA, 4.5S RNA [Escherichia coli O157:H7 EDL933] dbj|BAB38062.1| ribonuclease P protein component [Escherichia coli O157:H7] Length = 119

5039.2 Best-BlastP=> nrprot 62% Identities = 38/68 (55%), Positives = 51/68 (75%) ref|ZP_00134326.1| COG0759: Uncharacterized conserved protein [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 100

5040.2 Best-BlastP=> nrprot 68% Identities = 268/565 (47%), Positives = 381/565 (67%), Gaps = 23/565 (4%) ref|NP_820897.1| inner-membrane protein, 60kDa [Coxiella burnetii RSA 493] sp|P45650|60IM_COXBU 60 kDa inner-membrane protein homolog gb|AAO91411.1| inner-membrane protein, 60kDa [Coxiella burnetii RSA 493] Length = 566

5041.2 Best-BlastP=> nrprot 98% Identities = 176/178 (98%), Positives = 176/178 (98%) ref|O34955|PYR_LEGPN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) gb|AAB84257.1| inorganic pyrophosphatase [Legionella pneumophila] gb|AAC02428.1| inorganic pyrophosphatase [Legionella pneumophila] Length = 178

5042.1 Best-BlastP=> nrprot No Hits found

5043.3 Best-BlastP=> nrprot 70% Identities = 210/415 (50%), Positives = 298/415 (71%), Gaps = 2/415 (0%) ref|NP_760503.1| Putative Mg2+ and Co2+ transporter CorB [Vibrio vulnificus CMCP6] gb|AAO10030.1|AE016802_73 Putative Mg2+ and Co2+ transporter CorB [Vibrio vulnificus CMCP6] Length = 425

5044.2 Best-BlastP=> nrprot 73% Identities = 166/299 (55%), Positives = 217/299 (72%), Gaps = 13/299 (4%) ref|NP_763465.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08455.1|AE016813_207 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 304

5046.2 Best-BlastP=> nrprot 53% Identities = 45/118 (38%), Positives = 73/118 (61%), Gaps = 5/118 (4%) ref|XP_132330.1| RIKEN cDNA 2810006K23 [Mus musculus] gb|AAH46909.1| Similar to RIKEN cDNA 2810006K23 gene [Mus musculus] Length = 184

5047.3 Best-BlastP=> nrprot 41% Identities = 43/167 (25%), Positives = 80/167 (47%), Gaps = 6/167 (3%) ref|ZP_00067126.1| COG3009: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] Length = 217

5050.3 Best-BlastP=> nrprot No Hits found

5050.2 Best-BlastP=> nrprot 99% Identities = 241/243 (99%), Positives = 242/243 (99%) emb|CAD90952.1| LssA protein [Legionella pneumophila] Length = 243

5052.4 Best-BlastP=> nrprot 97% Identities = 194/201 (96%), Positives = 197/201 (98%) emb|CAD90953.1| LssZ protein [Legionella pneumophila] Length = 204

5054.2 Best-BlastP=> nrprot 33% Identities = 77/161 (47%), Positives = 108/161 (67%) ref|NP_390248.1| yqkA [Bacillus subtilis] sp|P54564|YQKA_BACSU Hypothetical protein yqkA_pir||C69966 hypothetical protein yqkA - Bacillus subtilis dbj|BAA12633.1| YqkA [Bacillus subtilis] emb|CAB14299.1| yqkA [Bacillus subsp. subtilis str. 168] Length = 343

5056.2 Best-BlastP=> nrprot 59% Identities = 57/101 (56%), Positives = 67/101 (66%), Gaps = 1/101 (0%) ref|ZP_00091135.1| COG2852: Uncharacterized protein conserved in bacteria [Azotobacter vinelandii] Length = 150

5058.2 Best-BlastP=>>nrprot 57% Identities = 29/66 (43%), Positives = 46/66 (69%), Gaps = 1/66 (1%) dbj|BAA75251.1| Similar to |S1301 of *Neisseria meningitidis* [Actinobacillus actinomycetemcomitans] Length = 255

5059.3 Best-BlastP=>>nrprot 44% Identities = 33/70 (47%), Positives = 46/70 (65%) pir|S61903 hypothetical protein 1 - *Neisseria meningitidis* emb|CAA88914.1| orf1 [Neisseria meningitidis] Length = 151

506.3 Best-BlastP=>>nrprot No Hits found

5060.2 Best-BlastP=>>nrprot 99% Identities = 504/505 (99%), Positives = 504/505 (99%) emb|CAB65195.1| hypothetical protein [Legionella pneumophila] Length = 505

5061.4 Best-BlastP=>>nrprot 87% Identities = 468/562 (83%), Positives = 492/562 (87%), Gaps = 16/562 (2%) emb|CAB65194.1| hypothetical protein [Legionella pneumophila] Length = 548

5062.3 Best-BlastP=>>nrprot 18% Identities = 24/71 (33%), Positives = 39/71 (54%) gb|AA21525.1| melitin-1 Length = 259

5064.2 Best-BlastP=>>nrprot No Hits found

5065.2 Best-BlastP=>>nrprot 34% Identities = 30/100 (30%), Positives = 54/100 (54%), Gaps = 11/100 (11%) ref|NP_593310.1| F-box protein [Schizosaccharomyces pombe] spj|P87053|POF1_SCHPO F-box/WD-repeat protein pof1 (Skp1-binding protein 1) pir|T38932 probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe) emb|CAB08168.1| SPAC57A10.05c [Schizosaccharomyces pombe] dbj|BA8484528.1| Pof1 [Schizosaccharomyces pombe] Length = 605

5066.2 Best-BlastP=>>nrprot 57% Identities = 50/121 (41%), Positives = 80/121 (66%), Gaps = 5/121 (4%) ref|NP_487806.1| two-component response regulator [Nostoc sp. PCC 7120] pir|AG2276 two-component response regulator all3766 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB75465.1| two-component response regulator [Nostoc sp. PCC 7120] Length = 143

5068.3 Best-BlastP=>>nrprot 51% Identities = 52/194 (26%), Positives = 98/194 (50%), Gaps = 8/194 (4%) ref|ZP_00110196.1| hypothetical protein [Nostoc punctiforme] Length = 223

5069.3 Best-BlastP=>>nrprot 53% Identities = 48/149 (32%), Positives = 74/149 (49%), Gaps = 25/149 (16%) ref|NP_812673.1| arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482] gb|AAO78867.1| arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482] Length = 157

507.3 Best-BlastP=>>nrprot 46% Identities = 18/32 (56%), Positives = 22/32 (68%) gb|AAN04217.1| putative transposase Tnp [Aeromonas salmonicida] Length = 383

5071.2 Best-BlastP=>>nrprot No Hits found

5072.2 Best-BlastP=>>nrprot 26% Identities = 30/85 (35%), Positives = 41/85 (48%) ref|NP_473229.2| putative protein kinase [Plasmodium falciparum 3D7] emb|CAA15620.3| putative protein kinase [Plasmodium falciparum 3D7] Length = 2515

5075.4 Best-BlastP=>>nrprot 11% Identities = 62/172 (36%), Positives = 102/172 (59%), Gaps = 18/172 (10%) ref|NP_703336.1| P. falciparum RESA-like protein with DnaJ domain [Plasmodium falciparum 3D7] emb|CAD48951.1| P. falciparum RESA-like protein with DnaJ domain [Plasmodium falciparum 3D7] Length = 1451

5076.2 Best-BlastP=>>nrprot 54% Identities = 50/158 (31%), Positives = 87/158 (55%), Gaps = 10/158 (6%) ref|NP_634196.1| Hydrogenase expression/formation protein [Methanosaerina mazei] pir|CAA62962.1| F420-nonreducing hydrogenase II [Methanosaerina mazei] Length = 161

5077.3 Best-BlastP=>>nrprot 60% Identities = 198/424 (46%), Positives = 262/424 (61%), Gaps = 2/424 (0%) ref|ZP_00089783.1| COG3259: Coenzyme F420-reducing hydrogenase, alpha subunit [Azotobacter vinelandii] Length = 442

5078.2 Best-BlastP=>>nprot 76% Identities = 250/432 (57%), Positives = 329/432 (76%), Gaps = 3/432 (0%) refINP_052842.1| hypothetical protein [Coxiella burnetii] gb|AAD33508.1|AF131076_34 hypothetical protein [Coxiella burnetii] Length = 433

5080.4 Best-BlastP=>>nprot 44% Identities = 121/443 (27%), Positives = 217/443 (48%), Gaps = 26/443 (5%) refINP_903425.1| probable peptide transporter protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61417.1| probable peptide transporter protein [Chromobacterium violaceum ATCC 12472] Length = 495

5081.3 Best-BlastP=>>nprot 50% Identities = 62/173 (35%), Positives = 96/173 (55%) refINP_520208.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD15794.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 194

5082.3 Best-BlastP=>>nprot No Hits found

5084.4 Best-BlastP=>>nprot 30% Identities = 94/351 (26%), Positives = 160/351 (45%), Gaps = 28/351 (7%) refINP_00087727.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 375

5087.2 Best-BlastP=>>nprot 19% Identities = 37/151 (24%), Positives = 69/151 (45%), Gaps = 11/151 (7%) refINP_705411.1| hypothetical protein, conserved [Plasmodium falciparum 3D7] emb|CAD52648.1| hypothetical protein, conserved [Plasmodium falciparum 3D7] Length = 2533

5088.2 Best-BlastP=>>nprot 53% Identities = 49/131 (37%), Positives = 76/131 (58%), Gaps = 4/131 (3%) refINP_832446.1| Acetyltransferase [Bacillus cereus ATCC 14579] gb|AAP09647.1| Acetyltransferase [Bacillus cereus ATCC 14579] Length = 141

509.1 Best-BlastP=>>nprot 50% Identities = 69/172 (40%), Positives = 99/172 (57%), Gaps = 10/172 (5%) refINP_903527.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61519.2| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 576

5090.2 Best-BlastP=>>nprot 59% Identities = 148/359 (41%), Positives = 211/359 (58%), Gaps = 12/359 (3%) refINP_662343.1| glutamate 5-kinase [Chlorobium tepidum TLS] sp|Q8KCG4|PROB_CHLTE Glutamate 5-kinase (Gamma-glutamyl kinase) (GK) gb|AAM72685.1| glutamate 5-kinase [Chlorobium tepidum TLS] Length = 361

5092.3 Best-BlastP=>>nprot No Hits found

5093.3 Best-BlastP=>>nprot 52% Identities = 97/243 (39%), Positives = 128/243 (52%), Gaps = 2/243 (0%) refINP_820472.1| UDP-2,3-diacylgucosamine hydrolase [Coxiella burnetii RSA 493] gb|AAO90986.1| UDP-2,3-diacylgucosamine hydrolase [Coxiella burnetii RSA 493] Length = 243

5094.2 Best-BlastP=>>nprot 55% Identities = 93/209 (44%), Positives = 129/209 (61%), Gaps = 13/209 (6%) refINP_00085068.1| COG0850: Septum formation inhibitor [Pseudomonas fluorescens PfO-1] Length = 245

5097.1 Best-BlastP=>>nprot 46% Identities = 76/295 (25%), Positives = 139/295 (47%), Gaps = 7/295 (2%) refINP_355292.1| AGR_C_4240p [Agrobacterium tumefaciens] refINP_533007.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|D97640 hypothetical protein AGR_C_4240 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AE2863 conserved hypothetical protein Atu2334 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK88077.1| AGR_C_4240p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL43323.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 302

5098.2 Best-BlastP=>>nprot No Hits found

510.2 Best-BlastP=>>nprot No Hits found

5100.2 Best-BlastP=> >nrprot 42% Identities = 101/389 (25%), Positives = 173/389 (44%), Gaps = 16/389 (4%) ref|NP_444149.1| Y4xM [Rhizobium sp. NGR234] spl|P55705|Y4XM_RHISN HYPOTHETICAL TRANSPORT PROTEIN Y4XM gb|AAB91936.1| Y4xM [Rhizobium sp. NGR234] Length = 404

5103.4 Best-BlastP=> >nrprot 42% Identities = 25/61 (40%), Positives = 37/61 (60%), Gaps = 1/61 (1%) gb|AAG10082.1|AF295331_2 outer membrane lipoprotein Pop [Edwardsiella tarda] Length = 155

5104.3 Best-BlastP=> >nrprot 48% Identities = 203/509 (39%), Positives = 293/509 (57%), Gaps = 9/509 (1%) ref|NP_896011.1| FAD linked oxidase, N-terminal [Prochlorococcus marinus str. MIT 9313] emb|CAE22361.1| FAD linked oxidase, N-terminal [Prochlorococcus marinus str. MIT 9313] Length = 571

5106.3 Best-BlastP=> >nrprot 32% Identities = 54/242 (22%), Positives = 111/242 (45%), Gaps = 24/242 (9%) gb|EAA15516.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 585

5108.2 Best-BlastP=> >nrprot No Hits found

5113.3 Best-BlastP=> >nrprot No Hits found

5114.3 Best-BlastP=> >nrprot No Hits found

5115.2 Best-BlastP=> >nrprot 44% Identities = 77/284 (27%), Positives = 141/284 (49%), Gaps = 19/284 (6%) ref|ZP_00128740.1| COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Desulfovibrio desulfuricans G20] Length = 326

5116.3 Best-BlastP=> >nrprot 56% Identities = 71/173 (41%), Positives = 107/173 (61%) ref|NP_800289.1| hypothetical protein VPA0779 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62122.1| hypothetical protein [Vibrio parahaemolyticus] Length = 203

5123.3 Best-BlastP=> >nrprot 57% Identities = 44/78 (56%), Positives = 54/78 (69%) ref|NP_819379.1| DNA-binding protein Fis [Coxiella burnetii RSA 493] gb|AAO89893.1| DNA-binding protein Fis [Coxiella burnetii RSA 493] Length = 103

5124.3 Best-BlastP=> >nrprot 78% Identities = 96/151 (63%), Positives = 120/151 (79%) ref|NP_820809.1| ribose-phosphate pyrophosphokinase [Coxiella burnetii RSA 493] gb|AAO91323.1| ribose-phosphate pyrophosphokinase [Coxiella burnetii RSA 493] Length = 319

5127.4 Best-BlastP=> >nrprot 77% Identities = 117/162 (72%), Positives = 141/162 (87%) ref|ZP_00068148.1| COG0462: Phosphoribosylpyrophosphate synthetase [Micromonospora degradans 2-40] Length = 316

5129.4 Best-BlastP=> >nrprot 76% Identities = 607/1050 (57%), Positives = 799/1050 (76%), Gaps = 12/1050 (1%) ref|NP_773366.1| AcrB/AcrD/AcrF family protein [Bradyrhizobium japonicum] dbj|BAC51991.1| AcrB/AcrD/AcrF family protein [Bradyrhizobium japonicum USDA 110] Length = 1052

5132.3 Best-BlastP=> >nrprot No Hits found

5133.3 Best-BlastP=> >nrprot No Hits found

5134.4 Best-BlastP=> >nrprot 99% Identities = 308/309 (99%), Positives = 309/309 (100%) gb|AAN63820.1| lysophospholipase A [Legionella pneumophila] Length = 309

5135.2 Best-BlastP=> >nrprot No Hits found

514.5 Best-BlastP=> >nrprot 16% Identities = 124/559 (22%), Positives = 243/559 (43%), Gaps = 100/559 (17%) gb|AAB00143.1| putative Length = 1015

5146.2 Best-BlastP=> >nrprot 55% Identities = 154/418 (36%), Positives = 238/418 (56%), Gaps = 13/418 (3%) gb|AAC44538.1| ProP [Escherichia coli] Length = 500

5147.1 Best-BlastP=>>nprot No Hits found

5151.1 Best-BlastP=>>nprot 56% Identities = 109/295 (36%), Positives = 167/295 (56%), Gaps = 9/295 (3%) ref|NP_346934.1| MccF-like protein [Clostridium acetobutylicum] pir|G96935 mcccF-like protein [imported] - Clostridium acetobutylicum gbj|AAK78274.1|AE007544_3 MccF-like protein [Clostridium acetobutylicum] Length = 306

5152.1 Best-BlastP=>>nprot 55% Identities = 56/126 (44%), Positives = 72/126 (57%), Gaps = 2/126 (1%) ref|NP_107051.1| unknown protein [Mesorhizobium loti] dbj|BAB52837.1| unknown protein [Mesorhizobium loti] Length = 274

5153.1 Best-BlastP=>>nprot 97% Identities = 141/145 (97%), Positives = 142/145 (97%) gbj|AAK00280.1|AF288536_2 unknown [Legionella longbeachae] Length = 145

5154.2 Best-BlastP=>>nprot 93% Identities = 253/273 (92%), Positives = 259/273 (94%) gbj|AAK00279.1|AF288536_1 spectinomycin 3' adenylyltransferase [Legionella longbeachae] Length = 274

5156.1 Best-BlastP=>>nprot No Hits found

5159.2 Best-BlastP=>>nprot 62% Identities = 240/471 (50%), Positives = 313/471 (66%), Gaps = 7/471 (1%) ref|NP_900831.1| probable melitin resistance protein [Chromobacterium violaceum ATCC 12472] gbj|AAQ58836.1| probable melitin resistance protein [Chromobacterium violaceum ATCC 12472] Length = 495

5162.1 Best-BlastP=>>nprot No Hits found

5164.1 Best-BlastP=>>nprot No Hits found

5167.4 Best-BlastP=>>nprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gbj|AAP83334.1|AF469614_2 unknown [Francisella tularensis] subsp. tularensis] Length = 94

5173.1 Best-BlastP=>>nprot 41% Identities = 195/643 (30%), Positives = 282/643 (43%), Gaps = 44/643 (6%) ref|NP_251563.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|F83287 hypothetical protein PA2873 [imported] - Pseudomonas aeruginosa (strain PAO1) gbj|AGG06261.1|AE004713_10 hypothetical protein PA2873 [Pseudomonas aeruginosa PAO1] Length = 668

5174.2 Best-BlastP=>>nprot No Hits found

5176.1 Best-BlastP=>>nprot No Hits found

5177.2 Best-BlastP=>>nprot 41% Identities = 61/168 (36%), Positives = 95/168 (56%), Gaps = 1/168 (0%) ref|ZP_00144063.1| Outer membrane protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gbj|EAA24326.1| Outer membrane protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 202

5178.1 Best-BlastP=>>nprot 98% Identities = 162/163 (99%), Positives = 162/163 (99%) gbj|AAC38179.1| DotD [Legionella pneumophila] = 163

5180.1 Best-BlastP=>>nprot 98% Identities = 74/75 (98%), Positives = 75/75 (100%) gbj|AN17184.1|AF492466_2 ferrous iron transporter A [Legionella pneumophila] Length = 75

5188.2 Best-BlastP=>>nprot 70% Identities = 205/420 (48%), Positives = 305/420 (72%), Gaps = 2/420 (0%) ref|ZP_00025967.1| COG1301: Na+/H+-dicarboxylate symporters [Ralstonia metallidurans] Length = 467

5189.2 Best-BlastP=>>nprot No Hits found

519.3 Best-BlastP=>>nprot 99% Identities = 549/550 (99%), Positives = 549/550 (99%) pir|A41468 60K heat shock protein htpB - Legionella pneumophila Length = 550

5193.2 Best-BlastP=>>nrprot 10% Identities = 49/180 (27%), Positives = 75/180 (41%), Gaps = 40/180 (22%) ref|NP_229450.1| alpha-amylase, putative [Thermotoga maritima] pir|[G72227 hypothetical protein TM1650 - Thermotoga maritima (strain MSB8) gb|AAD36717.1|AE001807_8 alpha-amylase, putative [Thermotoga maritima] Length = 422

5194.1 Best-BlastP=>>nrprot 52% Identities = 74/157 (47%), Positives = 98/157 (62%), Gaps = 5/157 (3%) ref|ZP_00036504.1| COG0046: Phosphoribosylformylglycineamidine (FGAM) synthase, synthetase domain [Enterococcus faecium] Length = 738

5195.2 Best-BlastP=>>nrprot 69% Identities = 237/447 (53%), Positives = 312/447 (69%), Gaps = 4/447 (0%) ref|NP_718290.1| succinylarginine dihydrolase [Shewanella oneidensis MR-1] gb|AA555734.1|AE015710_2 succinylarginine dihydrolase [Shewanella oneidensis MR-1] Length = 444

52.1 Best-BlastP=>>nrprot 88% Identities = 52/66 (78%), Positives = 60/66 (90%) emb|CAB60050.1| lvc [Legionella pneumophila] Length = 67

520.1 Best-BlastP=>>nrprot 62% Identities = 67/139 (48%), Positives = 92/139 (66%) ref|NP_440670.1| hypothetical protein [Synechocystis sp. PCC 6803] sp|P73321|Y194_SYNY3 Hypothetical protein slr1894 pir|[S77503 hypothetical protein slr1894 - Synechocystis sp. (strain PCC 6803) dbj|BA17350.1| ORF_ID:slr1894-hypothetical protein [Synechocystis sp. PCC 6803] Length = 156

5200.2 Best-BlastP=>>nrprot 77% Identities = 489/756 (64%), Positives = 587/756 (77%), Gaps = 5/756 (0%) ref|NP_820975.1| DNA topoisomerase I [Coxiella burnetii RSA 493] gb|AAO91489.1| DNA topoisomerase I [Coxiella burnetii RSA 493] Length = 765

5201.2 Best-BlastP=>>nrprot 73% Identities = 122/217 (56%), Positives = 165/217 (76%), Gaps = 2/217 (0%) sp|O66188|SCNC_THITI Thiocyanate hydrolase gamma subunit dbj|BAA28288.1| thiocyanate hydrolase gamma subunit [Thiobacillus thioparus] Length = 243

5202.2 Best-BlastP=>>nrprot 55% Identities = 46/92 (50%), Positives = 57/92 (61%), Gaps = 2/92 (2%) sp|O66187|SCNA_THITI Thiocyanate hydrolase alpha subunit dbj|BAA28287.1| thiocyanate hydrolase alpha subunit [Thiobacillus thioparus] Length = 126

5204.2 Best-BlastP=>>nrprot 46% Identities = 56/110 (50%), Positives = 74/110 (67%), Gaps = 1/110 (0%) sp|O66186|SCNB_THITI Thiocyanate hydrolase beta subunit dbj|BAA28286.1| thiocyanate hydrolase beta subunit [Thiobacillus thioparus] Length = 157

5206.1 Best-BlastP=>>nrprot 73% Identities = 212/360 (58%), Positives = 272/360 (75%), Gaps = 2/360 (0%) ref|ZP_00138670.1| COG1706: Flagellar basal-body P-ring protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 440

5208.1 Best-BlastP=>>nrprot 55% Identities = 34/86 (39%), Positives = 57/86 (66%), Gaps = 1/86 (1%) ref|NP_924146.1| hypothetical protein gsl1200 [Gloebacter violaceus] dbj|BAC89141.1| gsl1200 [Gloebacter violaceus] Length = 96

521.2 Best-BlastP=>>nrprot 55% Identities = 239/722 (33%), Positives = 382/722 (52%), Gaps = 53/722 (7%) ref|NP_773225.1| bll6585 [Bradyrhizobium japonicum] dbj|BAC51850.1| bll6585 [Bradyrhizobium japonicum USDA 110] Length = 861

5216.2 Best-BlastP=>>nrprot 64% Identities = 127/282 (45%), Positives = 18/282 (64%), Gaps = 9/282 (3%) ref|NP_643189.1| pirin [Xanthomonas axonopodis pv. citri str. 306] gb|AAM37725.1| pirin [Xanthomonas axonopodis pv. citri str. 306] Length = 285

5217.1 Best-BlastP=>>nrprot 76% Identities = 78/118 (66%), Positives = 95/118 (80%) ref|ZP_00024696.1| COG1484: DNA replication protein [Ralstonia metallidurans] Length = 268

5219.1 Best-BlastP=>>nrprot 50% Identities = 98/254 (38%), Positives = 135/254 (53%), Gaps = 11/254 (4%) gb|AAM90719.1| TraN [Salmonella typhi] Length = 617

5220.1 Best-BlastP=>>nrprot 26% Identities = 41/119 (34%), Positives = 58/119 (48%), Gaps = 16/119 (13%) ref|NP_052852.1| hypothetical protein [Coxiella burnetii] pir|S52231 hypothetical protein 160 - Coxiella burnetii emb|CAA59944.1| orf 160 [Coxiella burnetii]
gb|AAD33484.1|AF131076_10 hypothetical protein [Coxiella burnetii] Length = 160

5224.2 Best-BlastP=>>nrprot No Hits found

5226.2 Best-BlastP=>>nrprot 76% Identities = 117/173 (67%), Positives = 138/173 (79%) ref|NP_744614.1| translation initiation factor IF-3 [Pseudomonas putida KT2440] pir|BAN68078.1|AE016439_13 translation initiation factor IF-3 [Pseudomonas putida KT2440] Length = 177

5227.2 Best-BlastP=>>nrprot 68% Identities = 34/63 (53%), Positives = 46/63 (73%), Gaps = 1/63 (1%) sp|P13069|RL35_BACST 50S ribosomal protein L35 pir|LR5BS35 ribosomal protein L35 - Bacillus stearothermophilus emb|CAA34313.1| unnamed protein product [Geobacillus stearothermophilus] Length = 66

5229.1 Best-BlastP=>>nrprot 81% Identities = 108/142 (76%), Positives = 118/142 (83%) ref|NP_230221.1| ribosomal protein L13 [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82308 ribosomal protein L13 VC0570 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AF93738.1| ribosomal protein L13 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 142

523.2 Best-BlastP=>>nrprot 48% Identities = 87/267 (32%), Positives = 144/267 (53%), Gaps = 1/267 (0%) ref|NP_252216.1| probable outer membrane protein [Pseudomonas aeruginosa PA01] pir|D83204 probable outer membrane protein PA3526 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG08914.1|AE004773_3 probable outer membrane protein precursor [Pseudomonas aeruginosa PA01] Length = 321

5232.1 Best-BlastP=>>nrprot 39% Identities = 94/302 (31%), Positives = 135/302 (44%), Gaps = 38/302 (12%) ref|ZP_00065012.1| COG0323: DNA mismatch repair enzyme (predicted ATPase) [Microbulbifer degradans 2-40] Length = 630

5238.1 Best-BlastP=>>nrprot 71% Identities = 266/495 (53%), Positives = 354/495 (71%), Gaps = 5/495 (1%) ref|ZP_00067387.1| COG0138: AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aifl) [Microbulbifer degradans 2-40] Length = 526

524.2 Best-BlastP=>>nrprot 69% Identities = 194/342 (56%), Positives = 241/342 (70%), Gaps = 2/342 (0%) ref|NP_820684.1| dihydroorotate, homodimeric type [Coxiella burnetii RSA 493] gb|AAO91198.1| dihydroorotate, homodimeric type [Coxiella burnetii RSA 493] Length = 351

5242.3 Best-BlastP=>>nrprot No Hits found

5243.2 Best-BlastP=>>nrprot No Hits found

5247.1 Best-BlastP=>>nrprot 40% Identities = 80/312 (25%), Positives = 141/312 (45%), Gaps = 26/312 (8%) ref|ZP_00110262.1| hypothetical protein [Nostoc punctiforme] Length = 348

5250.2 Best-BlastP=>>nrprot 86% Identities = 234/324 (72%), Positives = 280/324 (86%) ref|NP_819669.1| dehydrogenase, E1 component, beta subunit, putative [Coxiella burnetii RSA 493] gb|AAO90183.1| dehydrogenase, E1 component, beta subunit, putative [Coxiella burnetii RSA 493] Length = 326

5253.1 Best-BlastP=>>nrprot 62% Identities = 92/196 (46%), Positives = 132/196 (67%), Gaps = 3/196 (1%) ref|ZP_00090036.1| COG4445: Hydroxylase for synthesis of 2-methylthio-cis-ribozeatin in tRNA [Azotobacter vinelandii] Length = 200

5254.1 Best-BlastP=>>nrprot 53% Identities = 72/206 (34%), Positives = 121/206 (58%) ref|NP_820242.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90756.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 206

5255.1 Best-BlastP=>>nrprot 54% Identities = 132/378 (34%), Positives = 210/378 (55%), Gaps = 8/378 (2%) ref|ZP_00087763.1| COG1520: FOG: WD40-like repeat [Pseudomonas fluorescens F⁺O-1] Length = 440

5256.2 Best-BlastP=>>nrprot 98% Identities = 64/64 (100%), Positives = 64/64 (100%) gb|AAG40471.1| global regulator [Legionella pneumophila] Length = 64

526.2 Best-BlastP=>>nrprot 97% Identities = 202/207 (97%), Positives = 203/207 (98%) gb|AAM00600.1| Rnase T [Legionella pneumophila] Length = 207

5266.2 Best-BlastP=>>nrprot 39% Identities = 212/1088 (19%), Positives = 439/1088 (40%), Gaps = 185/1088 (17%) pir|T14867 interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| interaptin [Dictyostelium discoideum] Length = 1738

5268.2 Best-BlastP=>>nrprot 54% Identities = 56/183 (30%), Positives = 107/183 (58%), Gaps = 6/183 (3%) ref|NP_821059.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91573.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 192

5269.1 Best-BlastP=>>nrprot No Hits found

5270.2 Best-BlastP=>>nrprot No Hits found

5273.1 Best-BlastP=>>nrprot 55% Identities = 42/101 (41%), Positives = 61/101 (60%), Gaps = 3/101 (2%) ref|NP_820129.1| oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] gb|AAO90643.1| oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] Length = 669

5277.3 Best-BlastP=>>nrprot 60% Identities = 186/328 (56%), Positives = 235/328 (71%), Gaps = 5/328 (1%) ref|NP_901482.1| dihydroorotate oxidase [Chromobacterium violaceum ATCC 12472] gb|AAQ59486.1| dihydroorotate oxidase [Chromobacterium violaceum ATCC 12472] Length = 344

5278.3 Best-BlastP=>>nrprot No Hits found

528.2 Best-BlastP=>>nrprot 99% Identities = 200/201 (99%), Positives = 201/201 (100%) gb|AAM00601.1| peroxynitrite reductase [Legionella pneumophila] Length = 201

5282.3 Best-BlastP=>>nrprot 44% Identities = 20/54 (37%), Positives = 32/54 (59%) ref|ZP_00077653.1| COG0693: Putative intracellular protease/amidase [Methanoscarcina barkeri] Length = 209

5288.1 Best-BlastP=>>nrprot 60% Identities = 60/130 (46%), Positives = 83/130 (63%), Gaps = 4/130 (3%) pir|A60635 glutathione transferase (EC 2.5.1.18), fosfomycin-modifying - Escherichia coli plasmid pSU961 transposon Tr2921 gb|AAA98399.1| fosfomycin-resistance protein [Serratia marcescens] Length = 141

5289.2 Best-BlastP=>>nrprot 32% Identities = 49/169 (28%), Positives = 73/169 (43%), Gaps = 19/169 (11%) ref|NP_819837.1| aminoglycoside N(6)-acetyltransferase [Coxiella burnetii RSA 493] gb|AAO90351.1| aminoglycoside N(6)-acetyltransferase [Coxiella burnetii RSA 493] Length = 188

529.2 Best-BlastP=>>nrprot 99% Identities = 105/105 (100%), Positives = 105/105 (100%) gb|AAM00602.1| glutaredoxin-like protein [Legionella pneumophila] Length = 115

5295.1 Best-BlastP=>>nrprot 68% Identities = 218/435 (50%), Positives = 309/435 (71%) ref|NP_253162.1| PmbA protein [Pseudomonas aeruginosa PAO1] pir|B83086 PmbA protein PA4472 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07860.1|AE004861_1 PmbA protein [Pseudomonas aeruginosa PAO1] Length = 449

5297.2 Best-BlastP=>>nrprot No Hits found

530.3 Best-BlastP=>>nrprot 50% Identities = 75/162 (46%), Positives = 100/162 (61%), Gaps = 3/162 (1%) ref|ZP_00129339.1| hypothetical protein [Desulfovibrio desulfuricans G20] Length = 231

5307.3 Best-BlastP=>>nrprot 19% Identities = 64/234 (27%), Positives = 111/234 (47%), Gaps = 23/234 (9%) ref|NP_820063.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90577.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 468

5309.1 Best-BlastP=>>nrprot 84% Identities = 196/267 (73%), Positives = 234/267 (87%) ref|NP_743889.1| septum site-determining protein Mind [Pseudomonas putida KT2440] gb|AAN67353.1|AE016361_7 septum site-determining protein Mind [Pseudomonas putida KT2440] Length = 270

531.4 Best-BlastP=>>nrprot No Hits found

5311.1 Best-BlastP=>>nrprot 58% Identities = 43/94 (45%), Positives = 58/94 (61%) ref|ZP_00090060.1| COG0721: Asp-tRNAAsn/Glu-tRNAGln amidotransferase C subunit [Azotobacter vinelandii] Length = 146

5312.2 Best-BlastP=>>nrprot 99% Identities = 206/208 (99%) ref|AAF05324.2| unknown virulence protein [Legionella pneumophila] Length = 208

5313.1 Best-BlastP=>>nrprot 32% Identities = 28/91 (30%), Positives = 46/91 (50%), Gaps = 6/91 (6%) ref|NP_520202.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD15788.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 176

5316.1 Best-BlastP=>>nrprot 41% Identities = 200/203 (98%), Positives = 203/203 (100%) ref|AAF05325.1| unknown virulence protein [Legionella pneumophila] Length = 205

5317.2 Best-BlastP=>>nrprot 65% Identities = 94/204 (46%), Positives = 136/204 (66%), Gaps = 1/204 (0%) ref|ZP_00067804.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 206

5318.2 Best-BlastP=>>nrprot 34% Identities = 47/115 (40%), Positives = 72/115 (62%) ref|NP_790719.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54414.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 249

5319.1 Best-BlastP=>>nrprot No Hits found

532.2 Best-BlastP=>>nrprot 57% Identities = 132/383 (34%), Positives = 215/383 (56%), Gaps = 24/383 (6%) ref|NP_718711.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56155.1|AE015753_1 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 374

5321.1 Best-BlastP=>>nrprot 43% Identities = 27/53 (50%), Positives = 38/53 (71%), Gaps = 2/53 (3%) ref|NP_84173.1| conserved hypothetical protein [Pseudomonas aeruginosa] Length = 744

5322.1 Best-BlastP=>>nrprot 58% Identities = 36/102 (35%), Positives = 61/102 (59%), Gaps = 3/102 (2%) ref|NP_816469.1| conserved domain protein [Enterococcus faecalis V583] gb|AAO82539.1| conserved domain protein [Enterococcus faecalis V583] Length = 104

5324.1 Best-BlastP=>>nrprot 51% Identities = 72/194 (37%), Positives = 113/194 (58%), Gaps = 2/194 (1%) ref|NP_719033.1| AcrB/AcrD/AcrF family protein [Shewanella oneidensis MR-1] gb|AAN56477.1|AE015784_10 AcrB/AcrD/AcrF family protein [Shewanella oneidensis MR-1] Length = 1046

5328.1 Best-BlastP=>>nrprot 41% Identities = 34/123 (27%), Positives = 62/123 (50%), Gaps = 4/123 (3%) ref|NP_692567.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC13602.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 402

533.2 Best-BlastP=>>nrprot 64% Identities = 122/264 (46%), Positives = 172/264 (65%), Gaps = 8/264 (3%) ref|NP_246208.1| AroE [Pasteurella multocida] sp|P57932|AROE_PASMU Shikimate 5-dehydrogenase gb|AAK03355.1| AroE [Pasteurella multocida] Length = 269

5334.1 Best-BlastP=>>nrprot 32% Identities = 70/121 (57%), Positives = 83/121 (68%), Gaps = 9/121 (7%) gb|AAQ82687.1| Epa5p [Candida glabrata] Length = 1218

5337.1 Best-BlastP=>>nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP833334.1|AF469614_2 unknown [Francisella tularensis subsp. tularensis] Length = 94

5338.2 Best-BlastP=>>nrprot 30% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180

5340.1 Best-BlastP=>>nrprot 14% Identities = 40/136 (29%), Positives = 73/136 (53%), Gaps = 19/136 (13%) gb|AAA67447.1| P120 Length = 232

5341.1 Best-BlastP=>>nrprot No Hits found

5342.2 Best-BlastP=>>nrprot 60% Identities = 87/178 (48%), Positives = 113/178 (63%), Gaps = 5/178 (2%) ref|NP_819838.1| transcriptional regulator, TetR family [Coxiella burnetii RSA 493] gb|AO90352.1| transcriptional regulator, TetR family [Coxiella burnetii RSA 493] Length = 193

5344.2 Best-BlastP=>>nrprot 21% Identities = 36/77 (46%), Positives = 48/77 (62%), Gaps = 1/77 (1%) ref|ZP_00028865.1| hypothetical protein [Burkholderia fungorum] Length = 123

5349.3 Best-BlastP=>>nrprot 15% Identities = 65/306 (21%), Positives = 140/306 (45%), Gaps = 40/306 (13%) dbj|BAC86266.1| unnamed protein product [Homo sapiens] Length = 486

5354.3 Best-BlastP=>>nrprot No Hits found

5359.2 Best-BlastP=>>nrprot 43% Identities = 22/59 (37%), Positives = 36/59 (61%) ref|NP_637282.1| flagellar protein [Xanthomonas campestris] pv. campestris str. ATCC 33913 Length = 135

536.3 Best-BlastP=>>nrprot 69% Identities = 459/876 (52%), Positives = 600/876 (68%), Gaps = 23/876 (2%) ref|NP_744167.1| aminopeptidase N [Pseudomonas putida KT2440] gb|AAN67631.1|AE016392_12 aminopeptidase N [Pseudomonas putida KT2440] Length = 885

5360.2 Best-BlastP=>>nrprot No Hits found

5361.2 Best-BlastP=>>nrprot 68% Identities = 179/380 (47%), Positives = 261/380 (68%), Gaps = 3/380 (0%) ref|NP_746466.1| flagellar biosynthetic protein FlhB [Pseudomonas putida KT2440] gb|AAN69930.1|AE016632_1 flagellar biosynthetic protein FlhB [Pseudomonas putida KT2440] Length = 380

5369.2 Best-BlastP=> >nrprot 72% Identities = 47/68 (69%), Positives = 58/68 (85%) ref|NP_639162.1| 30S ribosomal protein S21 [Xanthomonas campestris pv. campestris str. ATCC 33913] ref|NP_644178.1| 30S ribosomal protein S21 [Xanthomonas axonopodis pv. citri str. 306] sp|Q8NL04|RS21_XANAC 30S ribosomal protein S21 gb|AAM38714.1| 30S ribosomal protein S21 [Xanthomonas axonopodis pv. citri str. 306] gb|AAM43491.1| 30S ribosomal protein S21 [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 71

5372 Best-BlastP=> >nrprot No Hits found

5370.1 Best-BlastP=> >nrprot 97% Identities = 142/147 (96%), Positives = 144/147 (97%), Gaps = 1/147 (0%) gb|AAB09541.1| LporfX Length = 146

5373.1 Best-BlastP=> >nrprot No Hits found

5376.2 Best-BlastP=> >nrprot 25% Identities = 185/917 (20%), Positives = 352/917 (38%), Gaps = 160/917 (17%) gb|EAA15312.1| hypothetical protein [Plasmidium yoelii yoelii] Length = 1527

5377.2 Best-BlastP=> >nrprot No Hits found

538.1 Best-BlastP=> >nrprot No Hits found

5380.3 Best-BlastP=> >nrprot 49% Identities = 52/160 (32%), Positives = 91/160 (56%), Gaps = 5/160 (3%) ref|NP_248967.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|D83612 hypothetical protein PA0276 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG03665.1|AE004465_11 hypothetical protein PA0276 [Pseudomonas aeruginosa PAO1] Length = 171

5381.1 Best-BlastP=> >nrprot No Hits found

5382.1 Best-BlastP=> >nrprot No Hits found

5386.1 Best-BlastP=> >nrprot 67% Identities = 170/327 (51%), Positives = 225/327 (68%), Gaps = 3/327 (0%) ref|NP_844883.1| oxidoreductase, NAD-binding [Bacillus anthracis str. Ames] gb|AAP26369.1| oxidoreductase, NAD-binding [Bacillus anthracis str. Ames] Length = 341

5387.1 Best-BlastP=> >nrprot 67% Identities = 128/249 (51%), Positives = 169/249 (67%), Gaps = 2/249 (0%) gb|AAM51645.1| putative transposase [Francisella tularensis subsp. tularensis] Length = 247

5388.1 Best-BlastP=> >nrprot No Hits found

539.3 Best-BlastP=> >nrprot 61% Identities = 107/144 (74%), Positives = 123/144 (85%) emb|CAB46580.1| IS1400 transposase B [Yersinia enterocolitica] Length = 294

5390.1 Best-BlastP=> >nrprot 41% Identities = 30/89 (33%), Positives = 51/89 (57%) ref|NP_716406.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN53851.1|AE015522_6 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 100

5391.2 Best-BlastP=> >nrprot 58% Identities = 192/471 (40%), Positives = 283/471 (60%), Gaps = 5/471 (1%) ref|NP_840383.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD84207.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 510

5398.3 Best-BlastP=> >nrprot 66% Identities = 173/351 (49%), Positives = 237/351 (67%) ref|ZP_00084264.1| COG4972: Tfp pilus assembly protein, ATPase PiM [Pseudomonas fluorescens PfO-1] Length = 354

540.3 Best-BlastP=> >nrprot 72% Identities = 58/101 (57%), Positives = 78/101 (77%) emb|CAB46580.1| IS1400 transposase B [Yersinia enterocolitica] Length = 294

5402.1 Best-BlastP=>>nrprot No Hits found

5404.2 Best-BlastP=>>nrprot No Hits found

5405.2 Best-BlastP=>>nrprot 98% Identities = 314/322 (97%), Positives = 319/322 (99%) gbl|AAM00613.1| chemiosmotic efflux system protein B-like protein [Legionella pneumophila] Length = 322

5406.1 Best-BlastP=>>nrprot 34% Identities = 109/300 (36%), Positives = 175/300 (58%), Gaps = 15/300 (5%) ref|NP_902623.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 1390

5412.1 Best-BlastP=>>nrprot 72% Identities = 190/322 (59%), Positives = 232/322 (72%), Gaps = 6/322 (1%) ref|NP_638907.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gbl|AAM42831.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 323

5413.1 Best-BlastP=>>nrprot No Hits found

5417.1 Best-BlastP=>>nrprot 59% Identities = 50/137 (36%), Positives = 82/137 (59%), Gaps = 9/137 (6%) ref|NP_487806.1| two-component response regulator [Nostoc sp. PCC 7120] pirl|AG2276 two-component response regulator all3766 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB75465.1| two-component response regulator [Nostoc sp. PCC 7120] Length = 143

5420.1 Best-BlastP=>>nrprot 49% Identities = 42/134 (31%), Positives = 67/134 (50%), Gaps = 20/134 (14%) gbl|AAH41716.1| Similar to myosin, heavy polypeptide 4, skeletal muscle [Xenopus laevis] Length = 1170

5421.1 Best-BlastP=>>nrprot No Hits found

5422.1 Best-BlastP=>>nrprot No Hits found

5423.1 Best-BlastP=>>nrprot 64% Identities = 36/75 (48%), Positives = 50/75 (66%) ref|NP_252731.1| exodeoxyribonuclease VII small subunit [Pseudomonas aeruginosa PA01] ref|ZP_00137487.1| COG1722: Exonuclease VII small subunit [Pseudomonas aeruginosa PA14] sp|Q9HWY5|EX7S_PSEAE Probable exodeoxyribonuclease VII small subunit (Exonuclease VII exodeoxyribonuclease VII small subunit PA4042 [imported] - exodeoxyribonuclease VII small subunit [Pseudomonas aeruginosa PA01] Length = 80

5424.2 Best-BlastP=>>nrprot No Hits found

5426.2 Best-BlastP=>>nrprot 71% Identities = 86/142 (60%), Positives = 109/142 (76%), Gaps = 2/142 (1%) ref|NP_820553.1| tolR protein [Coxiella burnetii RSA 493] Length = 147

5427.1 Best-BlastP=>>nrprot 68% Identities = 114/225 (50%), Positives = 154/225 (68%), Gaps = 4/225 (1%) ref|ZP_00082839.1| COG0811: Biopolymer transport proteins [Pseudomonas fluorescens PfO-1] Length = 231

5428.1 Best-BlastP=>>nrprot 53% Identities = 48/116 (41%), Positives = 70/116 (60%), Gaps = 1/116 (0%) ref|NP_404733.1| conserved hypothetical protein [Yersinia pestis] ref|NP_670358.1| hypothetical protein [Yersinia pestis KIM] pirl|AH0137 conserved hypothetical protein YPO1120 [imported] - Yersinia pestis (strain CO92) emb|CAC89963.1| conserved hypothetical protein [Yersinia pestis CO92] gbl|AAW86609.1|AE013907_3 hypothetical protein [Yersinia pestis KIM] Length = 133

5429.1 Best-BlastP=>>nrprot 56% Identities = 33/73 (45%), Positives = 45/73 (61%), Gaps = 2/73 (2%) ref|NP_819889.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gbl|AAO90403.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 82

543.1 Best-BlastP=>>nrprot No Hits found

5437.2 Best-BlastP=> >nrprot No Hits found

5438.1 Best-BlastP=> >nrprot 73% Identities = 114/187 (60%), Positives = 144/187 (77%) ref|ZP_00065453.1| COG1207: N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch 2-40] Length = 451

544.2 Best-BlastP=> >nrprot 76% Identities = 265/446 (59%), Positives = 337/446 (75%), Gaps = 5/446 (1%) ref|ZP_00138105.1| COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Pseudomonas aeruginosa PA14] Length = 597

5440.1 Best-BlastP=> >nrprot No Hits found

5446.3 Best-BlastP=> >nrprot 62% Identities = 188/449 (41%), Positives = 279/449 (62%), Gaps = 12/449 (2%) gb|AAP74578.1| kynurenine 3-monooxygenase [Polaribacter filamentus] Length = 469

5447.1 Best-BlastP=> >nrprot 51% Identities = 88/224 (39%), Positives = 129/224 (57%), Gaps = 8/224 (3%) ref|NP_484370.1| unknown protein [Nostoc sp. PCC 7120] pir|AE1847 hypothetical protein all0326 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB72284.1| ORF_ID:all0326~unknown protein [Nostoc sp. PCC 7120] Length = 224

5448.1 Best-BlastP=> >nrprot 35% Identities = 36/120 (30%), Positives = 61/120 (50%), Gaps = 7/120 (5%) sp|P45790|GSPC_AERYH GENERAL SECRETION PATHWAY PROTEIN C emb|CAA47125.1| ExeC [Aeromonas hydrophila] Length = 290

5453.2 Best-BlastP=> >nrprot 68% Identities = 171/344 (49%), Positives = 242/344 (70%), Gaps = 1/344 (0%) ref|NP_819316.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO89830.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 458

5455.1 Best-BlastP=> >nrprot 64% Identities = 71/152 (46%), Positives = 101/152 (66%) ref|ZP_00140766.1| COG5528: Predicted integral membrane protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 155

5456.1 Best-BlastP=> >nrprot 99% Identities = 225/226 (99%), Positives = 226/226 (100%) gb|AAQ18123.1| CpxR [Legionella pneumophila] Length = 226

5457.1 Best-BlastP=> >nrprot 57% Identities = 52/117 (44%), Positives = 77/117 (65%) ref|NP_384234.1| PUTATIVE CYTIDINE DEAMINASE PROTEIN [Sinorhizobium meliloti] emb|CAC41515.1| PUTATIVE CYTIDINE DEAMINASE PROTEIN [Sinorhizobium meliloti] Length = 152

5458.1 Best-BlastP=> >nrprot 53% Identities = 32/96 (33%), Positives = 52/96 (54%), Gaps = 2/96 (2%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180

5460.1 Best-BlastP=> >nrprot 56% Identities = 147/325 (45%), Positives = 206/325 (63%), Gaps = 10/325 (3%) ref|NP_189431.2| DegP protease [Arabidopsis thaliana] gb|AAK62640.1| K16N12.18 [Arabidopsis thaliana] gb|AAM47381.1| At3g27925|K16N12.18 [Arabidopsis thaliana] Length = 439

5462.2 Best-BlastP=> >nrprot 66% Identities = 270/541 (49%), Positives = 367/541 (67%), Gaps = 6/541 (1%) ref|NP_819168.1| penicillin-binding protein 3 [Coxiella burnetii RSA 493] gb|AAO89682.1| penicillin-binding protein 3 [Coxiella burnetii RSA 493] Length = 548

5467.1 Best-BlastP=> >nrprot No Hits found

5469.1	Best-BlastP=>nrprot 70% Rd] sp P44814 DTD_HAEIN D-tyrosyl-tRNA(Tyr) deacylase pir IE64156 hypothetical protein Hl0670 - Haemophilus influenzae (strain Rd KW20) pdb 1J7G A Chain A, Structure Of Yhz From Haemophilus Influenzae (Hl0670), A D- Tyr-Tma[Tyr] Deacylase gbl AAC22330.1 conserved hypothetical protein [Haemophilus influenzae Rd] Length = 144	Identities = 24/155 (43%), Positives = 40/55 (72%) ref NP_438830.1 hypothetical protein [Haemophilus influenzae Rd] sp P44814 DTD_HAEIN D-tyrosyl-tRNA(Tyr) deacylase pir IE64156 hypothetical protein Hl0670 - Haemophilus influenzae (strain Rd KW20) pdb 1J7G A Chain A, Structure Of Yhz From Haemophilus Influenzae (Hl0670), A D- Tyr-Tma[Tyr] Deacylase gbl AAC22330.1
5470.1	Best-BlastP=>nrprot 76% [Pseudomonas fluorescens PfO-1] Length = 145	Identities = 58/83 (69%), Positives = 65/83 (78%) ref ZP_00083364.1 COG1490: D-Tyr-tRNATyr deacylase
5471.2	Best-BlastP=>nrprot 59% dbj BAC51857.1 bsr6592 [Bradyrhizobium japonicum USDA 110] Length = 95	Identities = 30/57 (52%), Positives = 41/57 (71%) ref NP_773232.1 bsr6592 [Bradyrhizobium japonicum]
5473.1	Best-BlastP=>nrprot 73% hydroxyalkanoate synthetase [Burkholderia fungorum] Length = 642	Identities = 15/4270 (57%), Positives = 197/270 (72%), Gaps = 5/270 (1%) ref ZP_00029131.1 COG3243: Poly(3-
5474.2	Best-BlastP=>nrprot 42% acetyltransferase HPA2 and related acetyltransferases [Burkholderia fungorum] Length = 174	Identities = 44/134 (32%), Positives = 73/134 (54%), Gaps = 2/134 (1%) ref ZP_00027817.1 COG0454: Histone acetyltransferases [Burkholderia fungorum]
5476.1	Best-BlastP=>nrprot 54% [Vibrio vulnificus CMCP6] gbl AO08959.1 AE016798_119 HesB family protein Length = 107	Identities = 48/106 (45%), Positives = 67/106 (63%), Gaps = 1/106 (0%) ref NP_759432.1 HesB family protein [Vibrio vulnificus CMCP6] Length = 107
5477.1	Best-BlastP=>nrprot 57% [Haemophilus ducreyi] gbl AAP95411.1 DNA-binding protein [Haemophilus ducreyi] 35000HP1 Length = 98	Identities = 36/84 (42%), Positives = 55/84 (65%), Gaps = 1/84 (1%) ref NP_873022.1 DNA-binding protein [Haemophilus ducreyi] 35000HP1 Length = 98
5478.2	Best-BlastP=>nrprot 28% homeobox 1 (X-PITX-1) (xPitx1) gbl AAD45292.1 AF155206_1 homeodomain transcription factor Pitx-1 [Xenopus laevis] Length = 305	Identities = 30/102 (29%), Positives = 47/102 (46%), Gaps = 13/102 (12%) sp Q9W751 P X1_XENLA Pituitary
5479.2	Best-BlastP=>nrprot 51% [Synechococcus sp. PCC 7942] Length = 208	Identities = 62/169 (36%), Positives = 102/169 (60%), Gaps = 2/169 (1%) gbl AAN46162.1 unknown protein
548.3	Best-BlastP=>nrprot No Hits found	TPR repeat, SEL1 subfamily [Magnetococcus sp. MC-1] Length = 831
5481.1	Best-BlastP=>nrprot 50% Identities = 143/306 (46%), Positives = 192/306 (62%), Gaps = 1/306 (0%) ref ZP_00043253.1 COG0790: FOG:	Identities = 75/284 (26%), Positives = 124/284 (43%), Gaps = 17/284 (5%) sp O57809 1A1D_PYRHO Putative 1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase) pdb 1J0AA A Chain A, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0A B Chain B, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B A Chain A, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B B Chain B, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B C Chain C, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B D Chain D, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B E Chain E, Crystal Structure Analysis Of The Acc Deaminase Homologue
5482.2	Best-BlastP=>nrprot 41% Homologue pdb 1J0A B Chain B, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B A Chain A, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B B Chain B, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B C Chain C, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb 1J0B D Chain D, Crystal Structure Analysis Of The Acc Deaminase Homologue	Complexed With Inhibitor pdb 1J0B C Chain C, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B D Chain D, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B E Chain E, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B F Chain F, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B G Chain G, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B H Chain H, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B I Chain I, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B J Chain J, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B K Chain K, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B L Chain L, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B M Chain M, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B N Chain N, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B O Chain O, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B P Chain P, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B Q Chain Q, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B R Chain R, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B S Chain S, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B T Chain T, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B U Chain U, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B V Chain V, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B W Chain W, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B X Chain X, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B Y Chain Y, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B Z Chain Z, Crystal Structure Analysis Of The Acc Deaminase Homologue
5484.4	Best-BlastP=>nrprot No Hits found	Complexed With Inhibitor pdb 1J0B F Chain F, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B G Chain G, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B H Chain H, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B I Chain I, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B J Chain J, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B K Chain K, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B L Chain L, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B M Chain M, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B N Chain N, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B O Chain O, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B P Chain P, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B Q Chain Q, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B R Chain R, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B S Chain S, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B T Chain T, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B U Chain U, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B V Chain V, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B W Chain W, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B X Chain X, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B Y Chain Y, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb 1J0B Z Chain Z, Crystal Structure Analysis Of The Acc Deaminase Homologue

5489.2

Best-BlastP=>>nrprot 52% Identities = 64/189 (33%), Positives = 107/189 (56%), Gaps = 8/189 (4%) refNP_8822264.1| putative exported protein [Bordetella pertussis] refNP_886390.1| putative exported protein [Bordetella parapertussis] refNP_891381.1| putative exported protein [Bordetella bronchiseptica] emb|CAE44018.1| putative exported protein [Bordetella pertussis] emb|CAE35211.1| putative exported protein [Bordetella bronchiseptica] Length = 207

549.5 Best-BlastP=>>nrprot 27% Identities = 60/253 (23%), Positives = 108/253 (42%), Gaps = 12/253 (4%) refNP_638097.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42021.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 618

5492.2 Best-BlastP=>>nrprot 77% Identities = 105/178 (58%), Positives = 145/178 (81%) refNP_251274.1| CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase [Pseudomonas aeruginosa PA01] pir|B83322 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase PA2584 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG05972.1|AE004687_1 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase [Pseudomonas aeruginosa PA01] Length = 186

5496.2 Best-BlastP=>>nrprot 95% Identities = 168/175 (96%), Positives = 171/175 (97%) emb|CAB65201.1| hypothetical protein [Legionella pneumophila] Length = 356

5497.1 Best-BlastP=>>nrprot 98% Identities = 328/334 (98%), Positives = 330/334 (98%) emb|CAB65202.1| WecA protein [Legionella pneumophila] Length = 334

5498.1 Best-BlastP=>>nrprot 99% Identities = 317/318 (99%), Positives = 318/318 (100%) emb|CAB65203.1| hypothetical protein [Legionella pneumophila] Length = 318

5499.1 Best-BlastP=>>nrprot 99% Identities = 291/291 (100%), Positives = 291/291 (100%) emb|CAB65204.1| RmlA protein [Legionella pneumophila] Length = 291

55.1 Best-BlastP=>>nrprot 98% Identities = 125/128 (97%), Positives = 127/128 (99%) gb|AAM08236.1| LvrB [Legionella pneumophila] Length = 150

5500.1 Best-BlastP=>>nrprot 98% Identities = 484/494 (97%), Positives = 486/494 (98%), Gaps = 2/494 (0%) sp|Q9RDY2|G6P1 LEGPN Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (P GI) (Phosphohexose isomerase) (PHI) emb|CAB65205.1| Gpi protein [Legionella pneumophila] Length = 497

5504.4 Best-BlastP=>>nrprot No Hits found

551.2 Best-BlastP=>>nrprot 64% Identities = 122/243 (50%), Positives = 163/243 (67%), Gaps = 3/243 (1%) refZP_00039313.1| COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Xylella fastidiosa] Dixon Length = 245

5514.2 Best-BlastP=>>nrprot 32% Identities = 56/241 (23%), Positives = 110/241 (45%), Gaps = 36/241 (14%) gb|EAA16038.1| repeat organellar protein-related [Plasmidium yoelii yoelii] Length = 1441

5515.2 Best-BlastP=>>nrprot 78% Identities = 149/249 (59%), Positives = 197/249 (79%) refNP_251642.1| electron transfer flavoprotein beta-subunit [Pseudomonas aeruginosa PA01] pir|C83277 electron transfer flavoprotein beta-subunit PA2952 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG06340.1|AE004721_8 electron transfer flavoprotein beta-subunit [Pseudomonas aeruginosa PA01] Length = 249

5517.1 BestBlastP=>>nrprot 50% Identities = 47/123 (38%), Positives = 65/123 (52%), Gaps = 14/123 (11%) ref|ZP_00087881.1| COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Pseudomonas fluorescens PfO-1] Length = 138

5520.1 BestBlastP=>>nrprot 38% Identities = 31/125 (24%), Positives = 57/125 (45%), Gaps = 4/125 (3%) ref|NP_716604.1| hypothetical protein [Shewanella oneidensis MR-1] gb|AAN54049.1|AE015542_5 hypothetical protein [Shewanella oneidensis MR-1] Length = 474

5521.1 BestBlastP=>>nrprot 61% Identities = 47/133 (35%), Positives = 83/133 (62%), Gaps = 1/133 (0%) ref|NP_903590.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61581.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 144

5523.2 BestBlastP=>>nrprot 60% Identities = 157/327 (48%), Positives = 203/327 (62%), Gaps = 9/327 (2%) ref|ZP_00086640.1| COG1612: Uncharacterized protein required for cytochrome oxidase assembly [Pseudomonas fluorescens PfO-1] Length = 359

5524.1 BestBlastP=>>nrprot 43% Identities = 46/180 (25%), Positives = 76/180 (42%), Gaps = 25/180 (13%) ref|NP_800052.1| hypothetical protein VPA0542 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61885_1| hypothetical protein [Vibrio parahaemolyticus] Length = 178

5526.2 BestBlastP=>>nrprot 30% Identities = 42/141 (29%), Positives = 64/141 (45%), Gaps = 2/141 (1%) ref|ZP_00081004.1| COG3637: Opacity protein and related surface antigens [Geobacter metallireducens] Length = 219

5527.2 BestBlastP=>>nrprot 69% Identities = 91/170 (53%), Positives = 120/170 (70%) ref|NP_743494.1| UDP-N-acetyl/muramoylalanine--D-glutamate ligase [Pseudomonas putida KT2440] gb|AAN66958.1|AE016324_8 UDP-N-acetyl/muramoylalanine--D-glutamate ligase [Pseudomonas putida KT2440] Length = 450

5528.2 BestBlastP=>>nrprot 99% Identities = 239/239 (100%), Positives = 239/239 (100%) emb|CAB65196.1| hypothetical protein [Legionella pneumophila] Length = 239

553.1 BestBlastP=>>nrprot No Hits found

5530.2 BestBlastP=>>nrprot 68% Identities = 119/231 (51%), Positives = 161/231 (69%) ref|NP_767647.1| bli1007 [Bradyrhizobium japonicum] dbj|BAC46272.1|bli1007 [Bradyrhizobium japonicum USDA 110] Length = 345

5532.2 BestBlastP=>>nrprot 50% Identities = 86/270 (31%), Positives = 146/270 (54%), Gaps = 11/270 (4%) ref|ZP_00117263.1| COG3781: Predicted membrane protein [Cytophaga hutchinsonii] Length = 290

5533.2 BestBlastP=>>nrprot 43% Identities = 28/84 (33%), Positives = 35/84 (41%), Gaps = 16/84 (19%) gb|AAO52009.1| similar to exonuclease II [Schizosaccharomyces pombe] [Dictyostelium discoideum] Length = 1749

5534.2 BestBlastP=>>nrprot 98% Identities = 486/494 (98%), Positives = 489/494 (98%) gbl|AAK35046.1|AF330136_2 type II protein secretion ATPase LspE [Legionella pneumophila] Length = 494

5535.1 BestBlastP=>>nrprot No Hits found

5538.2 BestBlastP=>>nrprot 75% Identities = 95/159 (59%), Positives = 121/159 (76%), Gaps = 1/159 (0%) ref|NP_819315.1| single-strand binding protein [Coxiella burnetii RSA 493] gb|AAO89829.1| single-strand binding protein [Coxiella burnetii RSA 493] Length = 158

5539.1 BestBlastP=>>nrprot No Hits found

5540.1 Best-BlastP=> >nrprot 81% Identities = 90/126 (71%), Positives = 104/126 (82%) ref|NP_252927.1| 50S ribosomal protein L17 [Pseudomonas aeruginosa PA01] sp|O52761|RL17_PSEAE 50S ribosomal protein L17 pir|C83113 50S ribosomal protein L17 PA4237 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAC03117.1| ribosomal large subunit protein L17 [Pseudomonas aeruginosa] gb|AAG07625.1|AE004841_3 50S ribosomal protein L17 [Pseudomonas aeruginosa PAO1] Length = 129

5542.3 Best-BlastP=> >nrprot 70% Identities = 120/255 (47%), Positives = 183/255 (71%), Gaps = 1/255 (0%) ref|NP_831729.1| Aminoglycoside 6-adenyltransferase [Bacillus cereus ATCC 14579] gb|AAP08930.1| Aminoglycoside 6-adenyltransferase [Bacillus cereus ATCC 14579] Length = 290

5546.1 Best-BlastP=> >nrprot 73% Identities = 65/107 (60%), Positives = 79/107 (73%), Gaps = 1/107 (0%) ref|NP_820379.1| ErfK丫bis丫cfS丫nhG family protein [Coxiella burnetii RSA 493] gb|AAO090893.1| ErfK丫bis丫cfS丫nhG family protein [Coxiella burnetii RSA 493] Length = 175

5548.1 Best-BlastP=> >nrprot No Hits found

5549.2 Best-BlastP=> >nrprot 73% Identities = 134/229 (58%), Positives = 172/229 (75%), Gaps = 3/229 (1%) ref|P_00065236.1| COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Microbifiler degradans 2-40] Length = 238

555.2 Best-BlastP=> >nrprot 53% Identities = 110/317 (34%), Positives = 171/317 (53%), Gaps = 11/317 (3%) ref|NP_442295.1| hypothetical protein [Synechocystis sp. PCC 6803] sp|Q55724|Y644_SYNY3 Hypothetical protein srl0644 pir|S76519 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10365.1| ORF_ID:srl0644~hypothetical protein [Synechocystis sp. PCC 6803] Length = 355

5550.3 Best-BlastP=> >nrprot 80% Identities = 334/503 (66%), Positives = 412/503 (81%), Gaps = 2/503 (0%) ref|NP_819973.1| cytochrome d ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] gb|AAO90487.1| cytochrome d ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] Length = 521

5552.2 Best-BlastP=> >nrprot 75% Identities = 232/378 (61%), Positives = 287/378 (75%), Gaps = 2/378 (0%) gb|AAG01153.1|AF284438_4 cytochrome d oxidase subunit [Brucella melitensis biovar Abortus] Length = 384

5554.2 Best-BlastP=> >nrprot No Hits found

5555.2 Best-BlastP=> >nrprot No Hits found

5556.1 Best-BlastP=> >nrprot No Hits found

5557.2 Best-BlastP=> >nrprot 42% Identities = 113/561 (20%), Positives = 251/561 (44%), Gaps = 65/561 (11%) dbj|BAB40921.2| myosin heavy chain 2x [Bos taurus] Length = 1938

5559.3 Best-BlastP=> >nrprot No Hits found

5560.3 Best-BlastP=> >nrprot 54% Identities = 68/232 (29%), Positives = 116/232 (50%), Gaps = 21/232 (9%) ref|NP_923239.1| probable carbonyl reductase [Gloeo bacter violaceus] dbj|BAC88234.1| glt0293 [Gloeo bacter violaceus] Length = 243

5563.1 Best-BlastP=> >nrprot 54% Identities = 57/145 (39%), Positives = 84/145 (57%), Gaps = 3/145 (2%) ref|NP_841440.1| GCN5-related N-acetyltransferase [Nitrosomonas europaea ATCC 19718] emb|CAD85310.1| GCN5-related N-acetyltransferase [Nitrosomonas europaea ATCC 19718] Length = 157

5564.1 Best-BlastP=> >nrprot 81% Identities = 322/475 (67%), Positives = 387/475 (81%), Gaps = 2/475 (0%) ref|NP_819499.1| dihydrodilipoamide dehydrogenase [Coxiella burnetii RSA 493] gb|AAO90013.1| dihydrodilipoamide dehydrogenase [Coxiella burnetii RSA 493] Length = 474

5566.1 Best-BlastP=> >nrprot 75% Identities = 38/55 (69%), Positives = 45/55 (81%) ref|NP_523225.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD18817.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 72

5569.1 Best-BlastP=> >nrprot No Hits found

557.2 Best-BlastP=> >nrprot 75% Identities = 517/898 (57%), Positives = 675/898 (75%), Gaps = 15/898 (1%) ref|NP_820774.1| DNA polymerase I [Coxiella burnetii RSA 493] gb|AAO91288.1| DNA polymerase I [Coxiella burnetii RSA 493] Length = 895

5576.3 Best-BlastP=> >nrprot 26% Identities = 61/216 (28%), Positives = 87/216 (40%), Gaps = 25/216 (11%) ref|NP_662329.1| hypothetical protein [Chlorobium tepidum TLS] gb|AAM72671.1| hypothetical protein [Chlorobium tepidum TLS] Length = 325

558.2 Best-BlastP=> >nrprot 34% Identities = 31/95 (32%), Positives = 53/95 (55%), Gaps = 9/95 (9%) gb|AAM15532.1|AF482691_1 probable sensor/response regulator hybrid [Pseudomonas aeruginosa] Length = 469

5582.4 Best-BlastP=> >nrprot 88% Identities = 584/737 (79%), Positives = 653/737 (88%), Gaps = 3/737 (0%) gb|AAM00624.1| putative copper efflux ATPase [Legionella pneumophila] Length = 736

5584.2 Best-BlastP=> >nrprot 52% Identities = 188/189 (99%), Positives = 188/189 (99%) emb|CAC33489.1| hypothetical protein [Legionella pneumophila] Length = 189

5586.1 Best-BlastP=> >nrprot 37% Identities = 32/76 (42%), Positives = 48/76 (63%) ref|NP_217688.1| hypothetical protein Rv3172c [Mycobacterium tuberculosis H37Rv] ref|NP_337786.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] ref|NP_856842.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] pirl|B70948 hypothetical protein Rv3172c - Mycobacterium tuberculosis (strain H37Rv) emb|CAA16637.1| hypothetical protein Rv3172c [Mycobacterium tuberculosis H37Rv] gb|AAK47600.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] emb|CAD95289.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] Length = 160

5587.3 Best-BlastP=> >nrprot 61% Identities = 132/276 (47%), Positives = 173/276 (62%) ref|NP_229753.1| 4-hydroxybenzoate octaprenyltransferase [Vibrio cholerae (strain N16961 serogroup O1) pirl|C82365 4-hydroxybenzoate octaprenyltransferase V0094 [imported] - Vibrio cholerae O1 biovar eltor str. N16961] Length = 284

5588.2 Best-BlastP=> >nrprot 67% Identities = 33/98 (33%), Positives = 65/98 (66%), Gaps = 4/98 (4%) ref|NP_819561.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90075.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 96

559.2 Best-BlastP=> >nrprot 83% Identities = 78/107 (72%), Positives = 92/107 (85%) ref|NP_862496.1| hypothetical protein [Pseudomonas sp. ADP] gb|AAK50291.1|U66917_59 hypothetical protein [Pseudomonas sp. ADP] Length = 152

5592.2 Best-BlastP=> >nrprot 81% Identities = 150/229 (65%), Positives = 188/229 (82%) ref|ZP_00134926.1| COG0081: Ribosomal protein L1 [Actinobacillus pleuropneumoniae] serovar 1 str. 4074] Length = 229

5593.1 Best-BlastP=> >nrprot 40% Identities = 30/79 (37%), Positives = 45/79 (56%) ref|NP_755977.1| Hypothetical protein [Escherichia coli CFT073] gb|AN82551.1|AE016767_311 Hypothetical protein [Escherichia coli CFT073] Length = 144

5595.2 Best-BlastP=> >nrprot 72% Identities = 112/174 (64%), Positives = 127/174 (72%), Gaps = 18/174 (10%) ref|ZP_00123239.1| COG0049: Ribosomal protein S7 [Haemophilus somnus 129PT] ref|ZP_00131785.1| hypothetical protein [Haemophilus somnus 2336] Length = 156

5596.3 Best-BlastP=>>nrprot 90% Identities = 109/123 (88%), Positives = 115/123 (93%) ref|NP_799152.1| ribosomal protein S12 [Vibrio parahaemolyticus RIMD 2210633] sp|Q87L43|RS12_VIBPA 30S ribosomal protein S12 dbj|BAC61036.1| ribosomal protein S12 [Vibrio parahaemolyticus] Length = 124

5598.2 Best-BlastP=>>nrprot 66% Identities = 189/394 (47%), Positives = 264/394 (67%), Gaps = 2/394 (0%) ref|NP_820522.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] gb|AAO91036.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] Length = 426

5600.2 Best-BlastP=>>nrprot 72% Identities = 45/66 (68%), Positives = 55/66 (83%) ref|NP_747188.1| ribosomal protein L31 [Pseudomonas putida KT2440] gb|AAN70652.1|AE016709_4 ribosomal protein L31 [Pseudomonas putida KT2440] Length = 100

5602.3 Best-BlastP=>>nrprot 65% Identities = 60/155 (38%), Positives = 102/155 (65%), Gaps = 7/155 (4%) ref|NP_069835.1| conserved hypothetical protein [Archaeoglobus fulgidus DSM 4304] pirl|B69375 phosphohistidine phosphatase (EC3.1.3.-) sixA-related [similarity] - Archaeoglobus fulgidus gb|AAB90241.1| conserved hypothetical protein [Archaeoglobus fulgidus DSM 4304] Length = 151

5605.2 Best-BlastP=>>nrprot No Hits found

5606.2 Best-BlastP=>>nrprot No Hits found

5607.2 Best-BlastP=>>nrprot 64% Identities = 221/475 (46%), Positives = 306/475 (64%), Gaps = 6/475 (1%) ref|NP_654832.1| hypothetical protein predicted by GeneMark [Bacillus anthracis Ames] ref|NP_843400.1| alginate O-acetyltransferase, putative [Bacillus anthracis Ames] gb|AAP24886.1| alginate O-acetyltransferase, putative [Bacillus anthracis Ames] Length = 471

5609.1 Best-BlastP=>>nrprot 70% Identities = 60/84 (71%), Positives = 67/84 (79%) ref|NP_819512.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAQ90026.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 92

5611.3 Best-BlastP=>>nrprot 80% Identities = 305/432 (70%), Positives = 352/432 (81%), Gaps = 2/432 (0%) ref|NP_901046.1| probable ATPase associated with chromosome architecture [Chromobacterium violaceum ATCC 12472] gb|AAQ59051.1| probable ATPase associated with chromosome architecture [Chromobacterium violaceum ATCC 12472] Length = 443

5610.1 Best-BlastP=>>nrprot 60% Identities = 47/109 (43%), Positives = 67/109 (61%), Gaps = 1/109 (0%) ref|ZP_00092417.1| hypothetical protein [Azotobacter vinelandii] Length = 137

5611.1 Best-BlastP=>>nrprot 43% Identities = 35/61 (57%), Positives = 47/61 (77%) ref|ZP_00092427.1| hypothetical protein [Azotobacter vinelandii] Length = 838

5615.1 Best-BlastP=>>nrprot 67% Identities = 115/242 (47%), Positives = 150/242 (61%), Gaps = 31/242 (12%) ref|ZP_00090468.1| COG0582: Integrase [Azotobacter vinelandii] Length = 399

562.1 Best-BlastP=>>nrprot 59% Identities = 78/206 (37%), Positives = 120/206 (58%), Gaps = 6/206 (2%) ref|ZP_00091807.1| COG2834: Outer membrane lipoprotein-sorting protein [Azotobacter vinelandii] Length = 207

5620.3 Best-BlastP=>>nrprot 51% Identities = 28/61 (45%), Positives = 39/61 (63%) ref|NP_600458.1| predicted transcriptional regulator [Corynebacterium glutamicum ATCC 13032] dbj|BAB98628.1| Predicted transcriptional regulators [Corynebacterium glutamicum ATCC 13032] Length = 75

5621.1 Best-BlastP=>>nrprot 35% Identities = 72/345 (20%), Positives = 148/345 (42%), Gaps = 30/345 (8%) ref|ZP_00118987.1| COG0477: Permeases of the major facilitator superfamily [Cytophaga hutchinsonii] Length = 441

5623.2 Best-BlastP=>>nprot 24% Identities = 57/252 (22%), Positives = 114/252 (45%), Gaps = 15/252 (5%) refINP_484762.1| unknown protein [Nostoc sp. PCC 7120] pir||AE1896 hypothetical protein alr0719 [imported] - Nostoc sp. (strain PCC 7120) db||BAB72676.1| ORF_D:alr0719-unknown protein [Nostoc sp. PCC 7120] Length = 393

5626.2 Best-BlastP=>>nprot 56% Identities = 119/291 (40%), Positives = 169/291 (58%), Gaps = 10/291 (3%) refINP_00091084.1| COG0582: Integrase [Azotobacter vinelandii] Length = 287

5630.1 Best-BlastP=>>nprot 42% Identities = 47/154 (30%), Positives = 72/154 (46%), Gaps = 24/154 (15%) refINP_519620.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb||CAD15201.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 233

5633.2 Best-BlastP=>>nprot 68% Identities = 143/273 (52%), Positives = 190/273 (69%), Gaps = 1/273 (0%) refINP_790075.1| diaminopimelate epimerase [Pseudomonas syringae pv. tomato str. DC3000] sp||Q88B09|DAPF_PSESM Diaminopimelate epimerase (DAP epimerase) gb||AO53770.1| diaminopimelate epimerase [Pseudomonas syringae pv. tomato str. DC3000] Length = 276

5634.2 Best-BlastP=>>nprot 58% Identities = 16/32 (50%), Positives = 25/32 (78%) refINP_00068204.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 57

5636.1 Best-BlastP=>>nprot No Hits found

5637.1 Best-BlastP=>>nprot 58% Identities = 86/198 (43%), Positives = 126/198 (63%), Gaps = 4/198 (2%) refINP_840924.1| Phospholipase/Carboxylesterase [Nitrosomonas europaea ATCC 19718] emb||CAD84761.1| Phospholipase/Carboxylesterase [Nitrosomonas europaea ATCC 19718] Length = 224

5638.2 Best-BlastP=>>nprot 68% Identities = 417/792 (52%), Positives = 546/792 (68%), Gaps = 28/792 (3%) refINP_251305.1| cell division protein FtsK [Pseudomonas aeruginosa PA01] sp||Q9J0M3|FTSK_PSEAE DNA translocase ftsK_pir||E83318 cell division protein FtsK PA2615 [imported] - Pseudomonas aeruginosa (strain PAO1) gb||AAG06003.1|AE004690_3 cell division protein FtsK PA2615 [imported] - PAO1 Length = 811

5642.1 Best-BlastP=>>nprot No Hits found

5644.3 Best-BlastP=>>nprot 47% Identities = 193/498 (38%), Positives = 268/498 (53%), Gaps = 78/498 (15%) refINP_233251.1| hemagglutinin/protease [Vibrio cholerae O1 biovar eltor str. N16961] sp||P24153|HAPT_VBCH Hemagglutinin/proteinase precursor (HA/protease) (Vibriolysin) pir||A42358 vibriolysin (EC 3.4.24.-) precursor [validated] - Vibrio cholerae (strain N16961 serogroup O1) gb||AA27579.1| HA/protease gb||AF96763.1| hemagglutinin/protease [Vibrio cholerae O1 biovar eltor str. N16961] Length = 609

5645.2 Best-BlastP=>>nprot 82% Identities = 520/752 (69%), Positives = 622/752 (82%), Gaps = 9/752 (1%) refINP_251310.1| ATP-binding protease component ClpA [Pseudomonas aeruginosa PA01] pir||B83319 ATP-binding proteinase component ClpA PA2620 [imported] - Pseudomonas aeruginosa (strain PAO1) gb||AAG06008.1|AE004690_8 ATP-binding protease component ClpA [Pseudomonas aeruginosa PAO1] Length = 758

5647.1 Best-BlastP=>>nprot 62% Identities = 55/80 (68%), Positives = 70/80 (87%) refINP_642326.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] sp||Q8PL06|CLPS_XANAC ATP-dependent Clp protease adaptor protein clpS_gbl|AM36862.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 106

5648.1 Best-BlastP=>>nrprot 60% Identities = 42/112 (37%), Positives = 68/112 (60%) ref|NP_753425.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN79985.1|AE016759_259 Hypothetical protein [Escherichia coli CFT073] Length = 393

5649.1 Best-BlastP=>>nrprot 88% Identities = 327/418 (78%), Positives = 371/418 (88%) ref|NP_746141.1| isocitrate dehydrogenase, NADP-dependent, prokaryotic-type [Pseudomonas putida KT2440] gb|AAN69605.1|AE016594_2 isocitrate dehydrogenase, NADP-dependent, prokaryotic-type [Pseudomonas putida KT2440] Length = 418

5650.3 Best-BlastP=>>nrprot 45% Identities = 67/239 (28%), Positives = 107/239 (44%), Gaps = 43/239 (17%) ref|NP_924301.1| unknown protein [Gloeobacter violaceus] dbj|BAC89296.1| gil1355 [Gloeobacter violaceus] Length = 278

5652.2 Best-BlastP=>>nrprot No Hits found

5654.2 Best-BlastP=>>nrprot No Hits found

5655.2 Best-BlastP=>>nrprot 58% Identities = 73/131 (55%), Positives = 94/131 (71%) ref|ZP_00108601.1| COG2193: Bacterioferritin (cytochrome b1) [Nostoc punctiforme] Length = 144

5656.2 Best-BlastP=>>nrprot 15% Identities = 23/70 (32%), Positives = 37/70 (52%), Gaps = 1/70 (1%) ref|NP_171674.2| expressed protein [Arabidopsis thaliana] pir|F86147 hypothetical protein T1N6_5 [imported] - Arabidopsis thaliana gb|AAF78398.1|AC009273_4 Contains similarity to a putative protein T2J13.100 gb|6522560 from Arabidopsis thaliana BAC T2J13 gb|AL132967 Length = 308

5660.1 Best-BlastP=>>nrprot 37% Identities = 69/275 (25%), Positives = 124/275 (45%), Gaps = 24/275 (8%) ref|NP_692096.1| hypothetical protein [Oceanobacillus iheyensis HTE831] dbj|BAC13131.1| hypothetical conserved protein [Oceanobacillus iheyensis HTE831] Length = 314

5662.1 Best-BlastP=>>nrprot 65% Identities = 92/150 (61%), Positives = 116/150 (77%) ref|NP_819966.1| conserved hypothetical protein [Coxiella burnetii RSA 4931] gb|AAQ090480.1| conserved hypothetical protein [Coxiella burnetii RSA 4931] Length = 414

5668.2 Best-BlastP=>>nrprot 28% Identities = 100/406 (24%), Positives = 167/406 (41%), Gaps = 82/406 (20%) ref|NP_220907.1| unknown [Rickettsia prowazekii] pir|E71657 hypothetical protein RP534 - Rickettsia prowazekii emb|CAA14983.1| unknown [Rickettsia prowazekii] Length = 598

5669.2 Best-BlastP=>>nrprot 43% Identities = 125/540 (23%), Positives = 240/540 (44%), Gaps = 44/540 (8%) ref|ZP_00044012..1| hypothetical protein [Magnetococcus sp. MC-1] Length = 725

567.5 Best-BlastP=>>nrprot 46% Identities = 236/953 (24%), Positives = 425/953 (44%), Gaps = 81/953 (8%) ref|NP_052976.1| 93% identical to sp:TRG1_ECOLI(gp:FPLTRAH_3)TraG of plasmid F, responsible for pilus biogenesis and stabilization of mating pairs [Plasmid R100] gb|AAD28728.1|AF112468_7 inner membrane and periplasmic mating pair stabilization protein TraG [Salmonella typhimurium] dbj|BA78880.1| 93% identical to sp:TRG1_ECOLI(gp:FPLTRAH_3)TraG of plasmid F, responsible for pilus biogenesis and stabilization of mating pairs [Plasmid R100] Length = 940

5671.2 Best-BlastP=>>nrprot 74% Identities = 73/123 (59%), Positives = 94/123 (76%), Gaps = 3/123 (2%) ref|ZP_00122793.1| COG1607: Acyl-CoA hydrolase [Haemophilus somnius 129PT] ref|ZP_00133225.1| hypothetical protein [Haemophilus somnius 2336] Length = 154

5672.1 Best-BlastP=>>nrprot No Hits found

5675.2 Best-BlastP=>>nrprot 52% Identities = 113/338 (33%), Positives = 186/338 (55%), Gaps = 23/338 (6%) ref|NP_767510.1| bli0870 [Bradyrhizobium japonicum] dbj|BAC46135.1| bli0870 [Bradyrhizobium japonicum USDA 110] Length = 329

5677.2 Best-BlastP=>>nrprot 34% [Plasmidum yoelii yoelii] Identities = 42/164 (25%), Positives = 70/164 (42%), Gaps = 21/164 (12%) gbl|EAA222028.1| putative yir4 protein Length = 299

568.2 Best-BlastP=>>nrprot 83% carboxyltransferase component (subunits alpha and beta) [Geobacter metallireducens] Identities = 380/535 (71%), Positives = 448/535 (83%) ref|ZP_00082147.1| COG4799: Acetyl-CoA carboxylase, Length = 535

5685.2 Best-BlastP=>>nrprot 99% Identities = 405/410 (98%), Positives = 408/410 (99%) gbl|AAM00606.1| unknown [Legionella pneumophila] Length = 421

5686.2 Best-BlastP=>>nrprot 70% [Pseudomonas aeruginosa PA01] ref|ZP_00137402.1| COG1522: Transcriptional regulators [Pseudomonas aeruginosa aeruginosa (strain PAO1) gbl|AAG07352.1|AE004814_7] pirl|F83150 probable transcription regulator PA3965 [imported] - Pseudomonas aeruginosa (strain PAO1) Length = 169

5687.1 Best-BlastP=>>nrprot No Hits found

5688.2 Best-BlastP=>>nrprot 39% Identities = 38/170 (22%), Positives = 75/170 (44%), Gaps = 33/170 (19%) gbl|EAA16038.1| repeat organellar protein-related [Plasmidum yoelii yoelii] Length = 1441

569.2 Best-BlastP=>>nrprot 64% Identities = 136/258 (52%), Positives = 170/258 (65%), Gaps = 1/258 (0%) ref|ZP_00082146.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Geobacter metallireducens] Length = 263

5690.2 Best-BlastP=>>nrprot 70% Identities = 75/146 (51%), Positives = 99/146 (67%), Gaps = 9/146 (6%) ref|NP_641722.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] gbl|AAM36258.1| conserved hypothetical protein [Xanthomonas axonopodis axonopodis pv. citri str. 306] Length = 149

5694.2 Best-BlastP=>>nrprot 64% Identities = 70/152 (46%), Positives = 103/152 (67%), Gaps = 3/152 (1%) ref|NP_719482.1| mce-related protein [Shewanella oneidensis MR-1] gbl|AAN56926.1|AE015826_11 mce-related protein [Shewanella oneidensis MR-1] Length = 157

5695.1 Best-BlastP=>>nrprot 77% Identities = 152/259 (58%), Positives = 202/259 (77%) ref|NP_931230.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE16405.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii TTO1] Length = 260

5696.2 Best-BlastP=>>nrprot 77% Identities = 168/258 (65%), Positives = 205/258 (79%) ref|NP_794201.1| toluene tolerance ABC transporter, ATP-binding protein, putative [Pseudomonas syringae pv. tomato str. DC3000] gbl|AAO57896.1| toluene tolerance ABC transporter, ATP-binding protein, putative [Pseudomonas syringae pv. tomato str. DC3000] Length = 269

57.1 Best-BlastP=>>nrprot 96% Identities = 272/289 (94%), Positives = 279/289 (96%) gbl|AAM08235.1| LvrA [Legionella pneumophila] Length = 289

5701.2 Best-BlastP=>>nrprot 67% Identities = 179/375 (47%), Positives = 250/375 (66%), Gaps = 9/375 (2%) ref|NP_519920.1| PUTATIVE DIHYDROLIPOAMIDE ACETYLTRANSFERASE (COMPONENT E2 OF PYRUVATE DEHYDROGENASE COMPLEX) PROTEIN [Ralstonia solanacearum] emb|CAD15501.1| PUTATIVE DIHYDROLIPOAMIDE ACETYLTRANSFERASE (COMPONENT E2 OF PYRUVATE DEHYDROGENASE COMPLEX) PROTEIN [Ralstonia solanacearum] Length = 372

571.2 Best-BlastP=>>nrprot 67% Identities = 336/671 (50%), Positives = 440/671 (65%), Gaps = 23/671 (3%) ref|ZP_00082145.1| COG4770: Acetyl/propionyl-CoA carboxylase, alpha subunit [Geobacter metallireducens] Length = 668

5711.2 Best-BlastP=>>nrprot No Hits found

5719.2 Best-BlastP=>>nrprot 66% Identities = 116/246 (47%), Positives = 167/246 (67%), Gaps = 1/246 (0%) ref|ZP_00123187.1| COG0149: Triosephosphate isomerase [Haemophilus somnis 129PT] Length = 255

572.2 Best-BlastP=>>nrprot 38% Identities = 161/480 (33%), Positives = 219/480 (45%), Gaps = 84/480 (17%) pir|UC4908 alkaline serine proteinase (EC 3.4.-.-) | precursor - Alteromonas sp Length = 715

5720.1 Best-BlastP=>>nrprot No Hits found

5723.1 Best-BlastP=>>nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP833334.1|AF469614_2 unknown [Francisella tularensis subsp. tularensis] Length = 94

5724.2 Best-BlastP=>>nrprot No Hits found

573.1 Best-BlastP=>>nrprot 79% Identities = 52/94 (55%), Positives = 75/94 (79%) ref|NP_820064.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAQ090578.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 94

5730.1 Best-BlastP=>>nrprot No Hits found

5735.2 Best-BlastP=>>nrprot 63% Identities = 181/388 (46%), Positives = 251/388 (64%), Gaps = 2/388 (0%) ref|NP_820522.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] gb|AAQ091036.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] Length = 426

5739.3 Best-BlastP=>>nrprot 31% Identities = 357/1425 (25%), Positives = 551/1425 (38%), Gaps = 320/1425 (22%) ref|NP_772111.1| bli5471 [Bradyrhizobium japonicum] dbj|BAC50736.1| bli5471 [Bradyrhizobium japonicum USDA 110] Length = 4210

574.2 Best-BlastP=>>nrprot No Hits found

5741.1 Best-BlastP=>>nrprot 60% Identities = 76/174 (43%), Positives = 116/174 (66%) ref|ZP_00043325.1| COG0398: Uncharacterized conserved protein [Magnetococcus sp. MC-1] Length = 222

5743.1 Best-BlastP=>>nrprot No Hits found

5747.1 Best-BlastP=>>nrprot No Hits found

5761.1 Best-BlastP=>>nrprot 25% Identities = 26/72 (36%), Positives = 38/72 (52%), Gaps = 1/72 (1%) ref|NP_902894.1| probable dehydrogenase [Chromobacterium violaceum ATCC 12472] gb|AAQ60890.1| probable dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 417

5765.1 Best-BlastP=>>nrprot 53% Identities = 39/100 (39%), Positives = 62/100 (62%) ref|NP_795325.1| ParB family protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO59020.1| ParB family protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 290

5766.1 Best-BlastP=>>nrprot 34% Identities = 39/142 (27%), Positives = 62/142 (43%), Gaps = 18/142 (12%) ref|NP_464180.1| Imo0653 [Listeria monocytogenes EGD-e] pir|AE1156 hypothetical protein [mo0653 [imported] - Listeria monocytogenes] Length = 306

5767.1 Best-BlastP=>>nrprot No Hits found

5769.2 Best-BlastP=>>nrprot 58% Identities = 52/126 (41%), Positives = 77/126 (61%), Gaps = 4/126 (3%) ref|NP_251491.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|A83296 hypothetical protein PA2801 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AG06189.1|AE004707_8 hypothetical protein PA2801 [Pseudomonas aeruginosa PAO1] Length = 134

577.2 Best-BlastP=>>nrprot 37% Identities = 58/180 (32%), Positives = 107/180 (59%), Gaps = 1/180 (0%) ref|NP_624053.1| predicted transposase [Thermoanaerobacter tengcongensis] gb|AM25657.1| predicted transposase [Thermoanaerobacter tengcongensis] Length = 267

5774.2 Best-BlastP=>>nrprot No Hits found

5776.1 Best-BlastP=>>nrprot No Hits found

5780.1 Best-BlastP=>>nrprot 61% Identities = 56/79 (70%), Positives = 63/79 (79%) ref|NP_246141.1| HisF [Pasteurella multocida] sp|Q9CLM0|HIS6_PASMU Imidazole glycerol phosphate synthase subunit hisF (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (IGPS subunit hisF) gb|AAK03288.1| HisF [Pasteurella multocida] Length = 256

5796.3 Best-BlastP=>>nrprot 46% Identities = 61/195 (31%), Positives = 92/195 (47%), Gaps = 26/195 (13%) ref|NP_890659.1| putative ring-hydroxylating dioxygenase large subunit [Bordetella bronchiseptica] emb|CAE34488.1| putative ring-hydroxylating dioxygenase large subunit [Bordetella bronchiseptica] Length = 438

58.1 Best-BlastP=>>nrprot 95% Identities = 211/227 (92%), Positives = 217/227 (92%) gb|AAM08234.1| putative phage repressor [Legionella pneumophila] Length = 227

5804.1 Best-BlastP=>>nrprot 53% Identities = 55/137 (40%), Positives = 76/137 (55%), Gaps = 12/137 (8%) ref|NP_229825.1| cytochrome c5 [Vibrio cholerae O1 biovar eltor str. N16961] pirl|F82355 cytochrome c5 VC0168 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93344.1| cytochrome c5 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 135

5806.2 Best-BlastP=>>nrprot 75% Identities = 54/87 (62%), Positives = 67/87 (77%) ref|ZP_00125359.1| COG0268: Ribosomal protein S20 [Pseudomonas syringae B728a] ref|NP_790649.1| ribosomal protein S20 [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54344.1| ribosomal protein S20 [Pseudomonas syringae pv. tomato str. DC3000] Length = 92

5807.1 Best-BlastP=>>nrprot 66% Identities = 48/113 (42%), Positives = 76/113 (67%) sp|Q43948|HYPA_AZOCH Hydrogenase nickel incorporation protein hypA (Protein hypA) pirl|JN0646 hydrogenase expression/formation protein HupA - Azotobacter chroococcum gb|AAA22132.1| hydrogenase accessory protein HupA Length = 113

5808.1 Best-BlastP=>>nrprot 48% Identities = 59/180 (32%), Positives = 87/180 (48%), Gaps = 13/180 (7%) gb|AAA25680.1| aminoglycoside 6-N-acetyltransferase Length = 180

5809.1 Best-BlastP=>>nrprot No Hits found

5812.1 Best-BlastP=>>nrprot 60% Identities = 57/154 (37%), Positives = 95/154 (61%), Gaps = 6/154 (3%) emb|CAB60049.1| lvrB [Legionella pneumophila] Length = 157

5813.1 Best-BlastP=>>nrprot 65% Identities = 30/57 (52%), Positives = 43/57 (75%) emb|CAB60050.1| lvrC [Legionella pneumophila] Length = 67

5814.1 Best-BlastP=>>nrprot 45% Identities = 38/121 (31%), Positives = 66/121 (54%), Gaps = 6/121 (4%) gb|AAL05416.1| PilL [Yersinia pseudotuberculosis] Length = 356

5816.1 Best-BlastP=>>nrprot 69% Identities = 52/96 (54%), Positives = 79/96 (82%) ref|ZP_00122751.1| COG0718: Uncharacterized protein conserved in bacteria [Haemophilus somnus 129PT] ref|ZP_00132634.1| hypothetical protein [Haemophilus somnus 2336] Length = 109

5818.1 Best-BlastP=>>nrprot No Hits found

5821.1 Best-BlastP=> >nrprot No Hits found

5822.1 Best-BlastP=> >nrprot No Hits found

5823.2 Best-BlastP=> >nrprot 49% Identities = 125/369 (33%), Positives = 198/369 (53%), Gaps = 33/369 (8%) ref|NP_899726.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] gb|AAQ57736.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] Length = 415

5824.1 Best-BlastP=> >nrprot 56% Identities = 43/67 (64%), Positives = 53/67 (79%) ref|NP_773113.1| b|6473 [Bradyrhizobium japonicum] dbj|BAC51738.1| b|6473 [Bradyrhizobium japonicum USDA 110] Length = 345

5829.2 Best-BlastP=> >nrprot 50% Identities = 67/218 (30%), Positives = 124/218 (56%), Gaps = 1/218 (0%) ref|NP_880554.1| putative glutamine-binding periplasmic protein precursor [Bordetella pertussis] emb|CAE42138.1| putative glutamine-binding periplasmic protein precursor [Bordetella pertussis] Length = 247

583.2 Best-BlastP=> >nrprot 82% Identities = 128/198 (64%), Positives = 164/198 (82%), Gaps = 1/198 (0%) ref|NP_743801.1| trp repressor binding protein [Pseudomonas putida KT2440] gb|AAN67265.1|AE016353_5 trp repressor binding protein [Pseudomonas putida KT2440] Length = 201

5844.1 Best-BlastP=> >nrprot 65% Identities = 66/135 (48%), Positives = 88/135 (65%), Gaps = 5/135 (3%) ref|NP_044227.1| KlcA [Enterobacter aerogenes] ref|NP_862440.1| KlcA protein [Pseudomonas sp. ADP] spl|P52602|KLA1_ECOLI Antirestriction protein klcA_pir|T08486 probable anti-restriction protein klcA - Enterobacter aerogenes plasmid R751 gb|AAC64430.1| KlcA [Enterobacter aerogenes] gb|AAK50236.1|U66917_3 KlcA protein [Pseudomonas sp. ADP] Length = 142

5846.2 Best-BlastP=> >nrprot No Hits found

5848.1 Best-BlastP=> >nrprot No Hits found

585.2

5844.1 Best-BlastP=> >nrprot 72% Identities = 62/118 (52%), Positives = 85/118 (72%), Gaps = 1/118 (0%) ref|NP_274848.1| conserved hypothetical protein [Neisseria meningitidis MC58] pir|A81035 conserved hypothetical protein NMB1852 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF42186.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 129

5856.1 Best-BlastP=> >nrprot 42% Identities = 20/43 (46%), Positives = 27/43 (62%), Gaps = 1/43 (2%) ref|ZP_00141162.1| COG0617: tRNA nucleotidyltransferase/poly(A) polymerase [Pseudomonas aeruginosa UCBPP-PA14] Length = 467

5857.1 Best-BlastP=> >nrprot 64% Identities = 65/139 (46%), Positives = 92/139 (66%) ref|NP_735626.1| Unknown [Streptococcus agalactiae NEM316] embl|CAD46839.1| Unknown [Streptococcus agalactiae NEM316] Length = 162

5867.1 Best-BlastP=> >nrprot No Hits found

587.2 Best-BlastP=> >nrprot 74% Identities = 149/254 (58%), Positives = 194/254 (76%), Gaps = 1/254 (0%) gb|EAA20230.1| exodeoxyribonuclease III [Plasmodium yoelii yoelii] Length = 271

5871.3 Best-BlastP=> >nrprot 46% Identities = 94/364 (25%), Positives = 174/364 (47%), Gaps = 21/364 (5%) ref|NP_691531.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] ref|NP_692364.1| hypothetical protein [Oceanobacillus iheyensis HTE831] ref|NP_693263.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC1256.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC13399.1| hypothetical conserved protein [Oceanobacillus iheyensis HTE831] dbj|BAC14298.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 402

5872.1 Best-BlastP=> >nrprot No Hits found

5874.1 Best-BlastP=> >nrprot 71% Identities = 96/178 (53%), Positives = 128/178 (71%), Gaps = 1/178 (0%) ref|ZP_00024697.1| COG4584:
Transposase and inactivated derivatives [Ralstonia metallidurans] Length = 343

5875.1 Best-BlastP=> >nrprot 43% Identities = 28/90 (31%), Positives = 44/90 (48%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii]
Length = 180

5876.2 Best-BlastP=> >nrprot 71% Identities = 121/219 (55%), Positives = 165/219 (75%), Gaps = 1/219 (0%) ref|NP_791574.1| cytidylate kinase
[Pseudomonas syringae pv. tomato str. DC3000] gb|AO55269.1| cytidylate kinase [Pseudomonas syringae pv. tomato str. DC3000]
Length = 229

588.3 Best-BlastP=> >nrprot 72% Identities = 146/252 (57%), Positives = 186/252 (73%) ref|NP_840124.1| Exodeoxyribonuclease
III:Exodeoxyribonuclease III xth [Nitrosomonas europaea ATCC 19718] emb|CAD83934.1| Exodeoxyribonuclease
III:Exodeoxyribonuclease III xth [Nitrosomonas europaea ATCC 19718] Length = 254

5890.1 Best-BlastP=> >nrprot No Hits found

5892.1 Best-BlastP=> >nrprot 73% Identities = 59/99 (59%), Positives = 73/99 (73%) ref|NP_742622.1| ribosomal protein L23 [Pseudomonas putida KT2440] gb|AAN66086.1|AE016238_4 ribosomal protein L23 [Pseudomonas putida KT2440] Length = 99

5894.3 Best-BlastP=> >nrprot 82% Identities = 202/275 (73%), Positives = 229/275 (83%) ref|ZP_00067989.1| COG0090: Ribosomal protein L2
[Microbulbifer degradans 2-40] Length = 275

5895.3 Best-BlastP=> >nrprot 86% Identities = 65/90 (72%), Positives = 80/90 (88%) ref|NP_882398.1| 30S ribosomal protein S19 [Bordetella parapertussis] ref|NP_886586.1| 30S ribosomal protein S19 [Bordetella bronchiseptica] emb|CAE39774.1| 30S ribosomal protein S19 [Bordetella parapertussis] emb|CAE30535.1| 30S ribosomal protein S19 [Bordetella bronchiseptica] Length = 91

5896.1 Best-BlastP=> >nrprot 62% Identities = 42/115 (36%), Positives = 75/115 (65%) ref|NP_286169.1| putative transport protein [Escherichia coli O157:H7 EDL933] ref|NP_308508.1| putative transport protein [Escherichia coli O157:H7] pir|A90689 probable transport protein ECs0481 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|E85539 probable transport protein yajR [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gb|AAG54777.1|AE005222_2 putative transport protein [Escherichia coli O157:H7 EDL933] dbj|BAB33904.1| putative transport protein [Escherichia coli O157:H7] Length = 456

5897.1 Best-BlastP=> >nrprot 55% Identities = 41/73 (56%), Positives = 51/73 (69%) ref|NP_931085.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] Length = 459

5898.2 Best-BlastP=> >nrprot 97% Identities = 266/271 (98%), Positives = 268/271 (98%) gb|AAC83338.1| major outer membrane protein precursor [Legionella pneumophila] gb|AAC83342.1| major outer membrane protein precursor [Legionella pneumophila] Length = 289

5899.1 Best-BlastP=> >nrprot No Hits found

59.1 Best-BlastP=> >nrprot 95% Identities = 137/145 (94%), Positives = 142/145 (97%) gb|AAM08233.1| unknown [Legionella pneumophila]
Length = 243

590.4 Best-BlastP=> >nrprot 17% Identities = 93/427 (21%), Positives = 182/427 (42%), Gaps = 50/427 (11%) ref|NP_603419.1| Exonuclease SBCC [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb|AAL94718.1| Exonuclease SBCC [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 921

5900.3 Best-BlastP=> >nrprot No Hits found

5901.3 Best-BlastP=>>nrprot 17% Identities = 49/177 (27%), Positives = 85/177 (48%), Gaps = 27/177 (15%) ref|NP_001259.1| RCC1-like G exchanging factor RLG [Homo sapiens] pir|T50663 RCC1-like G exchanging factor RLG [Imported] - human gb|AAC79987.1| RCC1-like G exchanging factor RLG [Homo sapiens] gb|AAH29052.1| RCC1-like G exchanging factor RLG [Homo sapiens] gb|AAP88928.1| chromosome condensation 1-like [Homo sapiens] Length = 551

5903.2 Best-BlastP=>>nrprot 76% Identities = 191/318 (60%), Positives = 247/318 (77%) ref|NP_819776.1| KpsF/GutQ family protein [Coxiella burnetii RSA 493] gb|AAO90290.1| KpsF/GutQ family protein [Coxiella burnetii RSA 493] Length = 324

5904.2 Best-BlastP=>>nrprot 21% Identities = 25/100 (25%), Positives = 46/100 (46%), Gaps = 6/100 (6%) ref|NP_283688.1| hypothetical protein NMA0899 [Neisseria meningitidis Z2491] pir|D81936 hypothetical protein NMA0899 [Imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB84177.1| hypothetical protein NMA0899 [Neisseria meningitidis Z2491] Length = 124

5905.1 Best-BlastP=>>nrprot 53% Identities = 118/304 (38%), Positives = 165/304 (54%), Gaps = 7/304 (2%) ref|NP_902888.1| probable translation initiation protein, Sua5/YciO/YrdC family [Chromobacterium violaceum ATCC 12472] gb|AAQ60884.1| probable translation initiation protein, Sua5/YciO/YrdC family [Chromobacterium violaceum ATCC 12472] Length = 321

5906.1 Best-BlastP=>>nrprot 100% Identities = 138/138 (100%), Positives = 138/138 (100%) emb|CAA67994.1| oxaloacetate decarboxylase alpha-chain [Legionella pneumophila] Length = 596

5907.1 Best-BlastP=>>nrprot 56% Identities = 20/31 (64%), Positives = 30/31 (96%) ref|NP_283131.1| hypothetical protein NMA0292 [Neisseria meningitidis Z2491] pir|G82024 hypothetical protein NMA0292 [Imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB83599.1| hypothetical protein NMA0292 [Neisseria meningitidis Z2491] Length = 94

591.3 Best-BlastP=>>nrprot 74% Identities = 156/258 (60%), Positives = 198/258 (76%) ref|ZP_00024696.1| COG1484: DNA replication protein [Ralstonia metallidurans] Length = 268

5910.1 Best-BlastP=>>nrprot No Hits found

592.3 Best-BlastP=>>nrprot 96% Identities = 531/559 (94%), Positives = 540/559 (96%) gb|AAM00619.1| unknown [Legionella pneumophila] Length = 559

5920.2 Best-BlastP=>>nrprot 46% Identities = 94/364 (25%), Positives = 174/364 (47%), Gaps = 21/364 (5%) ref|NP_691531.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] ref|NP_692364.1| hypothetical protein [Oceanobacillus iheyensis HTE831] ref|NP_693263.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC12566.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] hypothetical conserved protein [Oceanobacillus iheyensis HTE831] dbj|BAC14298.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 402

5926.1 Best-BlastP=>>nrprot 59% Identities = 3674 (48%), Positives = 4774 (63%) ref|NP_355900.1| AGR_L_236p [Agrobacterium tumefaciens] ref|NP_535243.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|C98145 hypothetical protein AGR_L_236 [Imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|A13142 conserved hypothetical protein Atu4765 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK88685.1| AGR_L_236p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AA45559.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 507

593.2 Best-BlastP=>>nrprot No Hits found

5935.1 Best-BlastP=>>nrprot No Hits found

594.1 Best-BlastP=>>nrprot 97% Identities = 145/150 (96%), Positives = 147/150 (98%) gbl|AAM00620.1| chemiosmotic efflux system C protein A [Legionella pneumophila] Length = 150

5944.1 Best-BlastP=>>nrprot No Hits found

5947.1 Best-BlastP=>>nrprot 65% Identities = 17/39 (43%), Positives = 30/39 (76%) ref|NP_469382.1| similar to *E. coli* DedA protein [Listeria innocua] pir||AD1437 *E. coli* DedA protein homolog lin0035 [imported] - *Listeria innocua* (strain Clip11262) emb|CAC95268.1| lin0035 [Listeria innocua] Length = 219

5950.1 Best-BlastP=>>nrprot No Hits found

5952.1 Best-BlastP=>>nrprot 79% Identities = 49/52 (94%), Positives = 49/52 (94%) gbl|AAM00633.1| unknown [Legionella pneumophila] Length = 176

5953.1 Best-BlastP=>>nrprot 87% Identities = 48/57 (84%), Positives = 50/57 (87%) spl|Q48815|HELA_LEGPN Protein helA gbl|AAB05679.1| HelA Length = 1052

5957.1 Best-BlastP=>>nrprot 68% Identities = 162/270 (60%), Positives = 214/270 (79%) ref|ZP_00122424.1| COG1185: Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase) [Haemophilus somnus 129PT] Length = 713

596.3 Best-BlastP=>>nrprot 73% Identities = 314/570 (55%), Positives = 419/570 (73%), Gaps = 5/570 (0%) ref|NP_819843.1| malate oxidoreductase [Coxiella burnetii] RSA 4931 gbl|AO90357.1| malate oxidoreductase [Coxiella burnetii] RSA 4931 Length = 565

597.2 Best-BlastP=>>nrprot 37% Identities = 29/80 (36%), Positives = 46/80 (57%), Gaps = 1/80 (1%) ref|NP_820267.1| hypothetical protein [Coxiella burnetii] RSA 4931 gbl|AO90781.1| hypothetical protein [Coxiella burnetii] RSA 4931 Length = 160

5978.2 Best-BlastP=>>nrprot 68% Identities = 92/166 (55%), Positives = 126/166 (75%) ref|NP_931234.1| hypothetical protein [Photorhabdus luminescens subsp. laumontii TTO1] emb|CAE16409.1| unnamed protein product [Photorhabdus luminescens subsp. laumontii TTO1] Length = 187

5979.1 Best-BlastP=>>nrprot No Hits found

598.2 Best-BlastP=>>nrprot 46% Identities = 36/101 (35%), Positives = 49/101 (48%), Gaps = 15/101 (14%) ref|NP_249404.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir||A83555 hypothetical protein PA0713 [imported] - *Pseudomonas aeruginosa* (strain PAO1) gbl|AG04102.1|AE004507.1 hypothetical protein PA0713 [Pseudomonas aeruginosa PAO1] Length = 97

5983.1 Best-BlastP=>>nrprot No Hits found

5985.1 Best-BlastP=>>nrprot 44% Identities = 29/106 (27%), Positives = 56/106 (52%), Gaps = 4/106 (3%) ref|NP_692567.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC13602.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 402

5986.2 Best-BlastP=>>nrprot No Hits found

5987.1 Best-BlastP=>>nrprot No Hits found

5988.1 Best-BlastP=>>nrprot 35% Identities = 27/55 (49%), Positives = 31/55 (56%), Gaps = 3/55 (5%) dbj|BAC94688.1| hypothetical protein [Vibrio vulnificus YJ016] Length = 343

5996.1 Best-BlastP=>>nrprot 51% Identities = 67/159 (42%), Positives = 90/159 (56%), Gaps = 3/159 (1%) ref|NP_742500.1| conserved hypothetical protein [Pseudomonas putida KT2440] gbl|AAN65964.1|AE016224.8 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 166

5999.1 Best-BlastP=>>nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614_2 unknown [Francisella tularensis
subsp. tularensis] Length = 94
Best-BlastP=>>nrprot No Hits found

60.1 Best-BlastP=>>nrprot 73% Identities = 117/172 (68%), Positives = 137/172 (79%) ref|NP_220600.1| ABC TRANSPORTER ATP-BINDING PROTEIN (abcT3) [Rickettsia prowazekii] pir|F71732 ABC transporter ATP-binding protein (abcT3) RP214 - Rickettsia prowazekii
emb|CAA14677.1| ABC TRANSPORTER ATP-BINDING PROTEIN (abcT3) [Rickettsia prowazekii] Length = 548

6002.1 Best-BlastP=>>nrprot 30% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1| ORF1 transposase
[Acinetobacter baumannii] Length = 180

6004.1 Best-BlastP=>>nrprot No Hits found

6007.1 Best-BlastP=>>nrprot No Hits found

601.4 Best-BlastP=>>nrprot 45% Identities = 97/361 (26%), Positives = 180/361 (49%), Gaps = 13/361 (3%) ref|NP_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589

6015.1 Best-BlastP=>>nrprot No Hits found

6016.1 Best-BlastP=>>nrprot 40% Identities = 31/71 (43%), Positives = 42/71 (59%), Gaps = 1/71 (1%) ref|NP_774998.1| putative protein [Citrobacter freundii] gb|AAN87662.1| putative protein [Citrobacter freundii] Length = 112

6018.1 Best-BlastP=>>nrprot No Hits found

6019.1 Best-BlastP=>>nrprot 56% Identities = 67/145 (46%), Positives = 100/145 (68%) ref|NP_635334.1| transcriptional regulator, AraC family [Methanoscarcina mazei Goe1] gb|AAM33006.1| transcriptional regulator, AraC family [Methanoscarcina mazei Goe1] Length = 209

602.4 Best-BlastP=>>nrprot 39% Identities = 64/253 (25%), Positives = 125/253 (49%), Gaps = 2/253 (8%) ref|NP_834835.1| Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] gb|AAP12036.1| Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] Length = 254

6029.1 Best-BlastP=>>nrprot 70% Identities = 31/48 (64%), Positives = 39/48 (81%) ref|NP_520567.1| PROBABLE 50S RIBOSOMAL SUBUNIT PROTEIN L33 [Ralstonia solanacearum] sp|Q8XWM8|RL33_RALSO 50S ribosomal protein L33 emb|CAD16153.1| PROBABLE 50S RIBOSOMAL SUBUNIT PROTEIN L33 [Ralstonia solanacearum] Length = 56

6036.1 Best-BlastP=>>nrprot 99% Identities = 110/110 (100%), Positives = 110/110 (100%) emb|CAC33488.1| hypothetical protein [Legionella pneumophila] Length = 110

6037.1 Best-BlastP=>>nrprot 47% Identities = 33/78 (42%), Positives = 54/78 (69%) sp|P04928|SANT_PLAFN S-ANTIGEN PROTEIN PRECURSOR pir|YAZQN7 S-antigen precursor - malaria parasite (Plasmodium falciparum) (strain NF7/Ghana) gb|AAA29758.1| S antigen precursor Length = 309

6038.1 Best-BlastP=>>nrprot No Hits found

6039.1

Best-BlastP=> >nrprot 82% Identities = 366/558 (65%), Positives = 460/558 (82%), Gaps = 3/558 (0%) ref|NP_251852.1| 30S ribosomal protein S1 [Pseudomonas aeruginosa PA01] pir|C83250 30S ribosomal protein S1 PA3162 [imported] - *Pseudomonas aeruginosa* (strain PAO1) gb|AAG06550.1|AE004740_3 30S ribosomal protein S1 [Pseudomonas aeruginosa PAO1] Length = 559

604.3 Best-BlastP=> >nrprot 55% Identities = 104/249 (41%), Positives = 138/249 (55%), Gaps = 6/249 (2%) ref|NP_419511.1| transcriptional regulator SkgA [Caulobacter crescentus CB15] sp|Q9R67|SKGA_CAUCR Transcriptional regulator skgA (Stationary-phase regulation of katG protein) pir|C87335 transcription regulator SkgA [imported] - *Caulobacter crescentus* gb|AAF01797.1|AF170912_1 putative helix-turn-helix transcriptional regulator SkgA [Caulobacter crescentus] gb|AAK22679.1| transcriptional regulator SkgA [Caulobacter crescentus CB15] Length = 255

6040.1 Best-BlastP=> >nrprot 71% Identities = 54/92 (58%), Positives = 72/92 (78%) ref|NP_819558.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA] 493] gb|AAO90072.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA] 493] Length = 438

6042.1 Best-BlastP=> >nrprot 69% Identities = 105/209 (50%), Positives = 149/209 (71%), Gaps = 2/209 (0%) ref|ZP_00122964.1| COG0125: Thymidylate kinase [Haemophilus somnis 129PT] Length = 210

6044.1 Best-BlastP=> >nrprot No Hits found

6049.1 Best-BlastP=> >nrprot 74% Identities = 123/208 (59%), Positives = 155/208 (74%), Gaps = 2/208 (0%) ref|NP_903586.1| probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] gb|AAQ61577.1| probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 539

6052.1 Best-BlastP=> >nrprot 47% Identities = 55/162 (33%), Positives = 91/162 (56%), Gaps = 2/162 (1%) ref|NP_719829.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN57273.1|AE015863_2 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 191

606.3

Best-BlastP=> >nrprot 56% Identities = 199/513 (38%), Positives = 301/513 (58%), Gaps = 6/513 (1%) ref|NP_819600.1| amino acid permease family protein [Coxiella burnetii RSA] 493] gb|AAO90114.1| amino acid permease family protein [Coxiella burnetii RSA] 493] Length = 560

6061.1 Best-BlastP=> >nrprot No Hits found

6062.1 Best-BlastP=> >nrprot 62% Identities = 75/166 (45%), Positives = 108/166 (65%), Gaps = 2/166 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180

6064.1 Best-BlastP=> >nrprot No Hits found

6066.1 Best-BlastP=> >nrprot 35% Identities = 34/122 (27%), Positives = 58/122 (47%), Gaps = 10/122 (8%) ref|NP_242278.1| transposase (01) [Bacillus halodurans] pir|D83826 transposase (01) BH1412 [imported] - *Bacillus halodurans* (strain C-125) dbj|BAB05131.1| transposase (01) [Bacillus halodurans] Length = 405

6070.1 Best-BlastP=> >nrprot 65% Identities = 59/121 (48%), Positives = 85/121 (70%) ref|NP_781505.1| 2-hydroxyacid dehydrogenase [Clostridium tetani E88] gb|AAO35442.1| 2-hydroxyacid dehydrogenase [Clostridium tetani E88] Length = 357

6071.1 Best-BlastP=> >nrprot 43% Identities = 23/67 (34%), Positives = 31/67 (46%) gb|AAK61303.1| putative transposase [Xanthomonas oryzae pv. oryzae] Length = 344

6072.1	Best-BlastP=>>nrprot 45%	Identities = 18/43 (41%), Positives = 29/43 (67%)	gb AAB38861.1 putative transposase [Burkholderia cepacia]
6074.1		Length = 345	
6079.1	Best-BlastP=>>nrprot 49% [Oceanobacillus iheyensis HTE831] ref NP_693308.1 transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj BAC14343.1 transposase for IS652 [Oceanobacillus iheyensis HTE831]	Identities = 48/175 (27%), Positives = 84/175 (48%), Gaps = 14/175 (8%)	ref NP_692337.1 transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj BAC13372.1 transposase for IS652 [Oceanobacillus iheyensis HTE831]
6079.1	Best-BlastP=>>nrprot 44%	Length = 722	Identities = 35/96 (36%), Positives = 49/96 (51%)
6081.1	Best-BlastP=>>nrprot 45%	Length = 337	Identities = 24/44 (54%), Positives = 32/44 (72%)
6083.1	Best-BlastP=>>nrprot No Hits found		Identities = 48/175 (27%), Positives = 84/175 (48%), Gaps = 14/175 (8%)
6086.1	Best-BlastP=>>nrprot 98%	Length = 121	Identities = 102/104 (98%), Positives = 103/104 (99%)
6087.1	Best-BlastP=>>nrprot No Hits found		gb AAM00607.1 unknown [Legionella pneumophila]
6089.1			
6093.1	Best-BlastP=>>nrprot 49% [Oceanobacillus iheyensis HTE831] ref NP_693308.1 transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj BAC14343.1 transposase for IS652 [Oceanobacillus iheyensis HTE831]	Identities = 48/175 (27%), Positives = 84/175 (48%), Gaps = 14/175 (8%)	ref NP_692337.1 transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj BAC13372.1 transposase for IS652 [Oceanobacillus iheyensis HTE831]
6094.1	Best-BlastP=>>nrprot No Hits found	Length = 1208	Identities = 1129/1221 (92%), Positives = 1163/1221 (95%), Gaps = 16/1221 (1%)
6097.1	Best-BlastP=>>nrprot 41% structural toxin protein RtxA [Legionella pneumophila]	Length = 1208	gb AAD41583.1 AF057703_1
6098.1	Best-BlastP=>>nrprot 50% methyltransferase [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE12382.1 DNA adenine methylase (Deoxyadenosyl-methyltransferase) [Photorhabdus luminescens subsp. laumondii TTO1]	Length = 270	Identities = 41/74 (55%), Positives = 53/74 (71%)
61.1	Best-BlastP=>>nrprot No Hits found		ref NP_927457.1 DNA adenine methylase (Deoxyadenosyl-methyltransferase)
6106.1	Best-BlastP=>>nrprot 37% [Deinococcus radiodurans] pirl A75633 probable transposase - Deinococcus radiodurans (strain R1)	Length = 327	Identities = 20/56 (35%), Positives = 32/56 (57%)
6107.1	Best-BlastP=>>nrprot No Hits found		ref NP_051664.1 transposase, putative [Deinococcus radiodurans]
6108.1	Best-BlastP=>>nrprot 63% [Acinetobacter baumannii]	Length = 180	Identities = 76/169 (44%), Positives = 110/169 (65%), Gaps = 2/169 (1%)
6110.1	Best-BlastP=>>nrprot 85%	Length = 356	gb AAF12606.1 AE001826_75 transposase, putative [Acinetobacter baumannii]
6117.1	Best-BlastP=>>nrprot 11% protein [Homo sapiens]	Length = 423	Identities = 74/77 (96%), Positives = 74/77 (96%)
			gb AN34371.1 ORF1 transposase [Legionella pneumophila]
			Length = 511/277 (18%)
			ref XP_300615.1 similar to hypothetical

6119.1 Best-BlastP=>nrprot 41% Identities = 34/123 (27%), Positives = 62/123 (50%), Gaps = 4/123 (3%) ref|NP_692567.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC13602.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 402

612.2 Best-BlastP=>nrprot 97% Identities = 696/721 (96%), Positives = 706/721 (97%) gb|AAC64361.1| catalase-peroxidase KatB [Legionella pneumophila] Length = 721

6121.1 Best-BlastP=>nrprot 52% Identities = 51/199 (25%), Positives = 100/199 (50%), Gaps = 21/199 (10%) gb|AAB05879.1| putative transposase Length = 424

6122.1 Best-BlastP=>nrprot No Hits found

6123.1 Best-BlastP=>nrprot No Hits found

6125.1 Best-BlastP=>nrprot 98% Identities = 51/51 (100%), Positives = 51/51 (100%) pir||T42167 Rep protein - Escherichia coli plasmid pO157 gb|AAC70135.1| Rep protein E1 [Escherichia coli O157:H7] Length = 51

6128.1 Best-BlastP=>nrprot 99% Identities = 388/388 (100%), Positives = 388/388 (100%) ref|NP_061425.1| 100 pct identical to gp:FPLMCG_6[SopA of plasmid F] [Plasmid F] gb|AAA24902.1| Protein A dbj|BAA97916.1| 100 pct identical to gp:FPLMCG_6[SopA of plasmid F] [Plasmid F] embl|CAC79981.1| orf1176 [Escherichia coli] gb|AAO61293.1| ParA [BAC cloning vector pEBAC190G] embl|CAD50597.1| SopA protein [Cloning vector pUvBBAC] Length = 391

6130.1 Best-BlastP=>nrprot 99% Identities = 323/323 (100%), Positives = 323/323 (100%) ref|NP_061426.1| 100 pct identical to sp:SPB_ECOLI[SopB of plasmid F] [Plasmid F] ref|NP_052641.1| SopB protein [Escherichia coli O157:H7] sp|P08867|SPPB_ECOLI SopB protein (Plasmid partition protein B) pir||T00244 sopB protein - Escherichia coli plasmids pO157 and F embl|CAA28296.1| unnamed protein product [Escherichia coli] gb|AA24903.1| Protein B gb|AAC53637.1| SopB dbj|BAA31791.1| SopB protein [Escherichia coli] gb|AAC70137.1| plasmid partitioning protein [Escherichia coli O157:H7] dbj|BAA97917.1| 100 pct identical to sp:SPPB_ECOLI[SopB of plasmid F] [Plasmid F] embl|CAC79980.1| orf972 [Escherichia coli] gb|AAO61294.1| ParB [BAC cloning vector pEBAC190G] embl|CAD50598.1| SopB protein [Cloning vector pUvBBAC] Length = 323

6131.1 Best-BlastP=>nrprot 47% Identities = 239/927 (25%), Positives = 368/927 (39%), Gaps = 188/927 (20%) ref|NP_772111.1| bli5471 [Bradyrhizobium japonicum] dbj|BAC50736.1| bli5471 [Bradyrhizobium japonicum USDA 110] Length = 4210

6132.1 Best-BlastP=>nrprot 37% Identities = 21/57 (36%), Positives = 33/57 (57%) ref|NP_051664.1| transposase, putative [Deinococcus radiodurans] pir||A75633 probable transposase - Deinococcus radiodurans (strain R1) gb|AAF12606.1|AE001826_75 transposase, putative [Deinococcus radiodurans] Length = 327

6133.1 Best-BlastP=>nrprot 67% Identities = 44/80 (55%), Positives = 59/80 (73%) ref|NP_273113.1| conserved hypothetical protein [Neisseria meningitidis MC58] pir||B81244 conserved hypothetical protein NMB0047 [Imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF40518.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 94

6134.1 Best-BlastP=>nrprot 54% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180

615.5 Best-BlastP=>nrprot 53% Identities = 58/230 (25%), Positives = 114/230 (49%), Gaps = 26/230 (11%) ref|NP_603496.1| Transposase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb|AAL94795.1| Transposase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 428

616.4 Best-BlastP=>>nrprot 67% Identities = 179/333 (53%), Positives = 231/333 (69%), Gaps = 4/333 (1%) refIZP_00024697.1| COG4584:
Transposase and inactivated derivatives [Ralstonia metallidurans] Length = 343

618.3 Best-BlastP=>>nrprot 55% Identities = 48/125 (38%), Positives = 77/125 (61%), Gaps = 2/125 (1%) refINP_867668.1| probable acyl carrier protein [Pirellula sp.] emb|CAD75215.1| probable acyl carrier protein [Pirellula sp.] Length = 129

619.1 Best-BlastP=>>nrprot 19% Identities = 32/118 (27%), Positives = 58/118 (49%), Gaps = 2/118 (1%) refINP_785252.1 (3R)-hydroxymyristoyl- [acyl carrier protein] dehydratase [Lactobacillus plantarum WCFS1] sp|Q88WGG9|FABZ_LACP1 (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase [Lactobacillus plantarum WCFS1] Length = 147

621.5 Best-BlastP=>>nrprot 62% Identities = 195/428 (45%), Positives = 269/428 (62%), Gaps = 17/428 (3%) refINP_214178.1| 3-oxoacyl-[acyl]-carrier protein synthase II [Aquifex aeolicus] pir|B70448 3-oxoacyl-[acyl]-carrier-protein synthase (EC 2.3.1.41) II - Aquifex aeolicus gb|AAC07574.1| 3-oxoacyl-[acyl]-carrier-protein synthase II [Aquifex aeolicus VF5] Length = 415

622.3 Best-BlastP=>>nrprot 69% Identities = 412/793 (51%), Positives = 556/793 (70%), Gaps = 12/793 (1%) refINP_820864.1| penicillin-binding protein 1A [Coxiella burnetii RSA 493] gb|AAO91378.1| penicillin-binding protein 1A [Coxiella burnetii RSA 493] Length = 793

623.2 Best-BlastP=>>nrprot 77% Identities = 253/370 (68%), Positives = 289/370 (78%) refIZP_00013240.1| COG0686: Alanine dehydrogenase [Rhodospirillum rubrum] Length = 372

627.1 Best-BlastP=>>nrprot 39% Identities = 110/214 (51%), Positives = 138/214 (64%), Gaps = 14/214 (6%) refINP_612899.1| hypothetical protein [Stx2 converting bacteriophage] dbj|BAB87868.1| hypothetical protein [Stx2 converting bacteriophage] Length = 678

628.3 Best-BlastP=>>nrprot No Hits found

631.1 Best-BlastP=>>nrprot 73% Identities = 577/1040 (55%), Positives = 773/1040 (74%), Gaps = 1/1040 (0%) refIZP_00055701.1| hypothetical protein [Magnetospirillum magnetotacticum] Length = 1059

632.2 Best-BlastP=>>nrprot 71% Identities = 136/258 (52%), Positives = 189/258 (73%), Gaps = 1/258 (0%) refINP_760580.1| Dihydropteroate synthase [Vibrio vulnificus CMCP6] gb|AAO10107.1|AE016802_150 Dihydropteroate synthase [Vibrio vulnificus CMCP6] Length = 259

633.3 Best-BlastP=>>nrprot 75% Identities = 282/442 (63%), Positives = 344/442 (77%), Gaps = 1/442 (0%) refINP_406959.1| probable phosphoglucomutase/phosphomannomutase [Yersinia pestis] refINP_668021.1| mrsA protein [Yersinia pestis KIM] pir|AE0425 probable phosphoglucomutase/phosphomannomutase [imported] - Yersinia pestis (strain CO92) emb|CAC92729.1| probable phosphoglucomutase/phosphomannomutase [Yersinia pestis CO92] gb|AAC84272.1|AE013670_9 mrsA protein [Yersinia pestis KIM] Length = 446

634.4 Best-BlastP=>>nrprot 51% Identities = 85/166 (51%), Positives = 93/166 (56%) emb|CAB44711.1| hypothetical protein (P4(21)n) [Mus musculus] Length = 400

635.5 Best-BlastP=>>nrprot 83% Identities = 278/398 (83%), Positives = 332/398 (83%), Gaps = 14/398 (3%) refINP_819191.1| cell division protein FtsZ [Coxiella burnetii RSA 493] gb|AAO89705.1| cell division protein FtsZ [Coxiella burnetii RSA 493] Length = 386

636.2 Best-BlastP=>>nrprot 77% Identities = 198/287 (68%), Positives = 236/287 (82%) refIZP_00090126.1| COG0774: UDP-3-O-acyl-N-acetylglucosamine deacetylase [Azotobacter vinelandii] Length = 303

637.3 Best-BlastP=> >nrprot 62% Identities = 261/623 (41%), Positives = 396/623 (63%), Gaps = 5/623 (0%) ref|NP_616924.1| endothelin converting enzyme homolog PepO [Methanoscarcina acetylorsans str. C2A] gb|AAM05404.1| endothelin converting enzyme homolog PepO [Methanoscarcina acetylorsans str. C2A] Length = 665

64.3 Best-BlastP=> >nrprot No Hits found

640.2 Best-BlastP=> >nrprot 51% Identities = 102/309 (33%), Positives = 157/309 (50%), Gaps = 8/309 (2%) ref|NP_103911.1| hypothetical protein [Mesorhizobium loti] dbj|BAB49697.1| hypothetical protein [Mesorhizobium loti] Length = 345

641.3 Best-BlastP=> >nrprot 74% Identities = 416/663 (62%), Positives = 506/663 (76%), Gaps = 5/663 (0%) ref|NP_931190.1| 2,4-dienoyl-CoA reductase [NADPH] (2,4-dienoyl coenzyme A reductase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16362.1| 2,4-dienoyl-CoA reductase [NADPH] (2,4-dienoyl coenzyme A reductase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 673

643.3 Best-BlastP=> >nrprot 59% Identities = 208/462 (45%), Positives = 287/462 (62%), Gaps = 10/462 (2%) ref|NP_284769.1| UDP-N-acetylglucosaminyl-tripeptide synthetase [Neisseria meningitidis] Z2491] sp|Q9JSZ0|MURE_NEIMA UDP-N-acetylglucosaminyl-D-glutamate-2,6-diaminopimelate ligase (UDP-N-acetylglucosaminyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-N-acetylglucosaminyl-D-glutamate-2,6-diamino-pimelate ligase (EC 6.3.2.13) NMA2071 [similarity] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB85288.1| UDP-N-acetylglucosaminyl-tripeptide synthetase [Neisseria meningitidis] Z2491] Length = 492

644.2 Best-BlastP=> >nrprot 52% Identities = 113/344 (32%), Positives = 185/344 (53%), Gaps = 10/344 (2%) ref|NP_820791.1| erythronate-4-phosphate dehydrogenase, putative [Coxiella burnetii] RSA 493] gb|AAO91305.1| erythronate-4-phosphate dehydrogenase, putative [Coxiella burnetii] RSA 493] Length = 375

645.4 Best-BlastP=> >nrprot 66% Identities = 107/219 (48%), Positives = 147/219 (67%), Gaps = 5/219 (2%) ref|NP_820725.1| membrane protein, putative [Coxiella burnetii] RSA 493] gb|AAO91239.1| membrane protein, putative [Coxiella burnetii] RSA 493] Length = 230

647.5 Best-BlastP=> >nrprot 49% Identities = 55/179 (30%), Positives = 107/179 (59%), Gaps = 1/179 (0%) gb|AAQ75156.1| Pap2 superfamily protein [Alvinella pompejana epibiont 7G3] Length = 202

651.1 Best-BlastP=> >nrprot No Hits found

650.3 Best-BlastP=> >nrprot 72% Identities = 211/372 (56%), Positives = 272/372 (73%), Gaps = 2/372 (0%) ref|ZP_00029745.1| COG2170: Uncharacterized conserved protein [Burkholderia fungorum] Length = 388

651.2 Best-BlastP=> >nrprot 73% Identities = 70/130 (53%), Positives = 98/130 (75%) ref|ZP_00079460.1| COG1832: Predicted CoA-binding protein [Geobacter metallireducens] Length = 136

652.1 Best-BlastP=> >nrprot 62% Identities = 144/267 (53%), Positives = 179/267 (67%), Gaps = 5/267 (1%) ref|NP_404647.1| conserved hypothetical protein [Yersinia pestis] ref|NP_670446.1| hypothetical protein [Yersinia pestis KIM] pirl|A10126 conserved hypothetical protein YPO1034 [imported] - Yersinia pestis (strain CO92) emb|CAC89876.1| conserved hypothetical protein [Yersinia pestis CO92] gb|AAM86697.1|AE0139_5_6 hypothetical protein [Yersinia pestis KIM] Length = 281

656.3 Best-BlastP=> >nrprot No Hits found

657.3 Best-BlastP=>>nrprot 6% Identities = 39/123 (31%), Positives = 64/123 (52%), Gaps = 11/123 (8%) ref|NP_828913.1| serine/threonine-protein kinase [Chlamydophila caviae GPIC] gb|AAP04791.1| serine/threonine-protein kinase [Chlamydophila caviae GPIC] Length = 501

659.2 Best-BlastP=>>nrprot 31% Identities = 56/209 (26%), Positives = 100/209 (47%), Gaps = 11/209 (5%) ref|NP_843168.1| conserved hypothetical protein [Bacillus anthracis str. Ames] gb|AAP24654.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 323

660.1 Best-BlastP=>>nrprot 61% Identities = 83/178 (46%), Positives = 117/178 (65%) ref|NP_794412.1| acetyltransferase, GNAT family [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58107.1| acetyltransferase, GNAT family [Pseudomonas syringae pv. tomato str. DC3000] Length = 189

661.3 Best-BlastP=>>nrprot 20% Identities = 51/148 (34%), Positives = 76/148 (51%), Gaps = 10/148 (6%) ref|ZP_00109305.1| COG1670: Acetyltransferases, including N-acetylases of ribosomal proteins [Nostoc punctiforme] Length = 191

663.2 Best-BlastP=>>nrprot 49% Identities = 193/671 (28%), Positives = 325/671 (48%), Gaps = 62/671 (9%) gb|AAL77346.1|AF443847_2 putative O-acetyltransferase WavN [Vibrio cholerae] Length = 663

665.2 Best-BlastP=>>nrprot 69% Identities = 43/78 (55%), Positives = 62/78 (79%) ref|NP_273842.1| conserved hypothetical protein [Neisseria meningitidis MC58] pirl|G81157 conserved hypothetical protein NMB0800 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF41213.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 94

666.2 Best-BlastP=>>nrprot 76% Identities = 120/204 (58%), Positives = 158/204 (77%) ref|ZP_00126281.1| COG0293: 23S rRNA methylase [Pseudomonas syringae pv. syringae B728a] Length = 216

667.3 Best-BlastP=>>nrprot 32% Identities = 68/178 (38%), Positives = 71/178 (39%) pirl|A40215 TcD antigen - Trypanosoma cruzi 207 Length = 207

668.4 Best-BlastP=>>nrprot 99% Identities = 1026/1048 (97%), Positives = 1040/1048 (99%) pirl|T18334 icmE protein - Legionella pneumophila emb|CAA75331.1| icmE protein [Legionella pneumophila] Length = 1048

670.1 Best-BlastP=>>nrprot 66% Identities = 213/471 (45%), Positives = 308/471 (65%), Gaps = 18/471 (3%) ref|ZP_00107537.1| COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, punctiforme] Length = 472

673.3 Best-BlastP=>>nrprot 42% Identities = 123/548 (22%), Positives = 218/548 (39%), Gaps = 102/548 (18%) ref|NP_458664.1| putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi] pirl|AI1031 probable membrane protein STY4579 [imported] - Salmonella enterica subsp. enterica serovar Typhi] gb|AAO71734.1| putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 501

675.6 Best-BlastP=>>nrprot No Hits found

677.6 Best-BlastP=>>nrprot 58% Identities = 258/683 (37%), Positives = 389/683 (56%), Gaps = 39/683 (5%) gb|AAN62290.1|AF440524_77 conserved hypothetical protein [Pseudomonas aeruginosa] Length = 724

678.3 Best-BlastP=>>nrprot No Hits found

680.3 Best-BlastP=>>nrprot 53% Identities = 57/132 (43%), Positives = 83/132 (62%), Gaps = 2/132 (1%) ref|NP_283256.1| patch repair protein [Neisseria meningitidis Z2491] sp|Q9JWD6|VSR_NEIMA Putative very-short-patch-repair endonuclease pir|[H81959 patch repair protein (EC 3.1.-.) NMA0429 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB83728.1| patch repair protein [Neisseria meningitidis Z2491] Length = 140

681.3 Best-BlastP=>>nrprot No Hits found

682.2 Best-BlastP=>>nrprot 76% Identities = 191/295 (64%), Positives = 229/295 (77%), Gaps = 7/295 (2%) sp|Q59603|MTB1_NEIGO Modification methylase NgoBI (Cytosine-specific methyltransferase [Neisseria gonorrhoeae]) Length = 317

683.2 Best-BlastP=>>nrprot 64% Identities = 200/443 (45%), Positives = 289/443 (65%), Gaps = 11/443 (2%) ref|NP_819174.1| UDP-N-acetylumuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase [Coxiella burnetii RSA 493] Length = 446 N-acetylumuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase [Coxiella burnetii RSA 493] Length = 446

684.5 Best-BlastP=>>nrprot 48% Identities = 73/253 (28%), Positives = 127/253 (50%), Gaps = 40/253 (15%) ref|NP_819573.1| cell division protein ZipA, putative [Coxiella burnetii RSA 493] sp|AAO90087.1| cell division protein ZipA, putative [Coxiella burnetii RSA 493] Length = 225

687.5 Best-BlastP=>>nrprot 47% Identities = 120/426 (28%), Positives = 204/426 (47%), Gaps = 29/426 (6%) ref|ZP_00082430.1| COG0304: 3-oxoacyl-(acyl-carrier-protein) synthase [Geobacter metallireducens] Length = 410

688.1 Best-BlastP=>>nrprot 48% Identities = 71/266 (26%), Positives = 138/266 (51%), Gaps = 11/266 (4%) ref|NP_908017.1| LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolinella succinogenes] emb|CAE10917.1| LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolinella succinogenes] Length = 300

692.1 Best-BlastP=>>nrprot No Hits found

693.1 Best-BlastP=>>nrprot 71% Identities = 96/172 (55%), Positives = 128/172 (74%) ref|NP_299266.1| conserved hypothetical protein [Xylella fastidiosa 9a5c] pir|[C82613 conserved hypothetical protein XF1984 [imported] - Xylella fastidiosa (strain 9a5c)] Length = 187

694.3 Best-BlastP=>>nrprot 72% Identities = 239/453 (52%), Positives = 330/453 (72%), Gaps = 9/453 (1%) dbj|BAB33285.1| glutathione reductase [Acinetobacter sp. M-1] Length = 450

696.2 Best-BlastP=>>nrprot 74% Identities = 92/143 (64%), Positives = 107/143 (74%), Gaps = 13/143 (9%) ref|NP_230222.1| ribosomal protein S9 [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KUF0|RS9_VIBCH 30S ribosomal protein S9 pir|[C82308 ribosomal protein S9 VC0571 [imported] - Vibrio cholerae (strain N16961 serogroup O1) dbj|AAF93739.1| ribosomal protein S9 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 130

697.1 Best-BlastP=>>nrprot 74% Identities = 111/188 (59%), Positives = 142/188 (75%), Gaps = 3/188 (1%) ref|NP_840883.1| Rieske iron-sulfur protein 2Fe-2S subunit [Nitrosomonas europaea ATCC 19718] Length = 201

698.2 Best-BlastP=>>nrprot 81% Identities = 273/401 (68%), Positives = 332/401 (82%) ref|NP_743478.1| ubiquinol--cytochrome c reductase, cytochrome b [Pseudomonas putida KT2440] sp|AAN66942.1|AE016322_9 ubiquinol--cytochrome c reductase, cytochrome b [Pseudomonas putida KT2440] Length = 403